

GenCore version 5.1.6  
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# OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 02:08:24 ; Search time 7208 Seconds  
(without alignments)  
13165.125 Million cell updates/sec

Title: US-10-089-612-2

Perfect score: 2493

Sequence: 1 aagctttccggtgatgaag.....aaatagcttcacagctaga 2493

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gse1.\*
- 9: gb\_gse2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713.2	28.6	956	9	CG165489 PUKD807B
2	626.8	25.1	704	8	CC431305 PUFPL91TD
3	620.6	24.9	958	8	BZ789069 PUFDF79TD
c 4	539.6	21.6	924	8	BZ789073 PUFDF79TD
5	379	15.2	555	8	BZ407849 OGAC134TM
c 6	355	14.2	578	8	BZ407846 OGAC134TC
c 7	328.6	13.2	1114	9	CL984849 ZMWBHD000
c 8	328.2	13.2	1062	9	CL987946 ZMWBHD000
c 9	311	12.5	1058	9	CL986825 ZMWBHD000
c 10	292.6	11.7	1035	9	CL986043 ZMWBHD000
11	282.8	11.3	917	9	CG171826 PUFPL91TD
12	281.6	11.3	808	9	CG204991 PUFY83TB
13	259.6	10.4	882	9	CG368356 OGXDR48TV
14	208.2	8.4	788	9	CG067437 PUIIR86TB
15	207.8	8.3	582	8	BZ312667 i27h06.b
c 16	203.8	8.2	760	9	CC997884 ZUAE557TH
c 17	182	7.3	910	8	BZ703611 PUBLV66TD
c 18	180.2	7.2	983	9	CL254917 ZMWBHD060
c 19	175.4	7.0	968	9	CG139245 PUKAP14TD
20	170.8	6.9	931	9	CG158928 PUFPR06TB
21	170.6	6.8	876	9	CG127109 PUFRC30TD
22	170.2	6.8	708	8	CC433252 PUKA077TB
23	168.8	6.8	1025	9	CG047285 PUKBJ77TD
24	168.4	6.8	905	8	CC434444 PUKNK90TD

c 25	155.6	6.2	514	8	BZ327501	BZ327501 i27h06.g
c 26	153.4	6.2	425	9	CC735092	CC735092 OGUG277TV
c 27	153.2	6.1	1038	9	CG420560	CG420560 ZMWBHD003
c 28	152.2	6.1	590	8	BZ678438	BZ678438 PUBC677TD
c 29	152.2	6.1	609	8	BZ376109	BZ376109 i665403.g
c 30	152.2	6.1	714	8	BZ671566	BZ671566 PUBC677TD
c 31	152.2	6.1	791	8	BZ372257	BZ372257 i665403.b
c 32	151.4	6.1	792	8	CC012679	CC012679 PUDHU26TD
c 33	146.6	5.9	579	8	BZ372153	BZ372153 i664003.b
c 34	143	5.7	508	8	BH784025	BH784025 fzab013f0
c 35	142.8	5.7	779	9	CG069355	CG069355 PUAAP91TD
c 36	141.6	5.7	929	9	CG139241	CG139241 PUKAP14TD
c 37	141.4	5.7	819	8	CC376588	CC376588 PUKX74TD
c 38	140.6	5.6	968	8	CC434443	CC434443 PUKNK90TB
c 39	139.4	5.6	860	9	CG368347	CG368347 OGXDR48TH
c 40	138.6	5.6	740	8	BZ982826	BZ982826 PUFJY05TD
c 41	138.6	5.6	890	8	CC386965	CC386965 PUDBO19TB
c 42	137.4	5.5	743	8	BZ756164	BZ756164 PUDBO19TB
c 43	135.2	5.4	853	8	BZ680379	BZ680379 PUBJ3C94TD
c 44	134.8	5.4	848	8	BZ756167	BZ756167 PUDBO19TD
c 45	125.2	5.0	1021	9	CG198973	CG198973 PUPZM68TB

## ALIGNMENTS

RESULT 1  
CG165489  
LOCUS  
DEFINITION  
CG165489 PUKD807B ZM\_0.6.1.0\_KB\_Zea mays genomic clone ZMBrTa0797M15,  
genomic survey sequence.  
ACCESSION  
CG165489  
VERSION  
CG165489.1  
KEYWORDS  
GSS:34056290  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 956)  
AUTHORS  
White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Renick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Bennetzen, J.  
TITLE  
Maize Genomics Consortium  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1..956  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
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/clone\_lib="ZM\_0.6.1.0\_KB"  
/note="Vector: PCR1-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
Cot selected genomic DNA library"

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

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Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..956

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone\_lib="ZMBrTa0797M15"

/clone\_lib="ZM\_0.6.1.0\_KB"

/note="Vector: PCR1-TOPO; Site 1: EcoRI; 0.6-1.0 kb high

Cot selected genomic DNA library"

Query Match 28.6%; Score 713.2; DB 9; Length 956;

Best Local Similarity 90.8%; Pred. No. 1.5e-156;

Matches 872; Conservative 0; Mismatches 73; Indels 15; Gaps 10;

Qy 1397 GGCGATGCTCTTTTATAGGG--AGCACCATTGATTAAT--GGAAGACATGACACAAG 1453

Db 3 GGCGTGGTCTCTTTTATAGGGCCACCAATTGATTAAATGGGAGACATGACAGAG 62

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Qy 1454 GCTGTGGGACAGCTTTAAAGCTCGAATCTGCTAGGGTGTCTCAAGGTTAAAGATACAGG 1513
Db 63 GGTGTGGGACAGCTTTAAAGCTCGAATCTGCTAGGGTGTCTCAAGGTTAAAGATACAGG 122
Qy 1514 CATCAGGGAGGAAAGGACAGGATAAAATTTCTTACTCCAGTGTGGGGTGATGGGGACA 1573
Db 123 CATCAGGGAGGAAAGGAGGATAAAATTTCTTACTCTAGTGTGGGGTGATGGGGACA 182
Qy 1574 AGGGTAGTGTCTCAAGCAAGGGGGGAGTTCAGCGAGATGCGCTGTGTGACACATG 1633
Db 183 AGGGTAGTGTCTCAAGCAAGGGGGGAGTTCAGCGAGATGCGCTGTGTGACACATG 242
Qy 1634 GGGGGGGGGAAATTGGAGGTGGGGTTGACCGAGTGAAGTATGCGCTGACCCAGAGAG 1693
Db 243 GGGGGGTGGG--AGTGGGAGGTTGAGGTTAAAGGTTGGGGTTATGGCTCAGCGAGAG-AG 299
Qy 1694 AGACCCAGCTGATGGGGAAGAGGTGCCACNGTGGGAGCCAGAGTGTCAAGTACTCAC 1753
Db 300 AGACCCAGCTGATGGGGGGGAGAGAA-GTGCCACAGAGTGGGGA-CGAGGTGTCAAGTACTCAC 357
Qy 1754 CGTGACATGTTATTTGGAAAGTTACGTCGGAAATGGTTTGGGCTGAGTGTAGGCTGG 1813
Db 358 GAGCACATGTTAGTGTGTAAGTGGGTGGGAAATGGTTTGGGCTGAGTGTAGGCTGG 417
Qy 1814 CTGGGCACTGTGCTGATCCTTTAATTTCTC---CATTTCCCAATTTTAAAGTTGAATTTT 1869
Db 418 CTGGGCACTGTGCTGATCCTTTAATTTCTC---CATTTCCCAATTTTAAAGTTGAATTTT 477
Qy 1870 AATTCAAATCAAATG-ACTCCAAATCTCTCC-AAAATTAACCAAAATATAGAATATTTAGA 1927
Db 478 AATTCAAATCAAATGAACTCCAAATCTCTCCAAATATTAACAAAATCTAGAATATTTAGA 537
Qy 1928 TGAATATGTTGGTGGAGTTTGGGCTCGGCTTTTGGTTAGTATGTTCTATATAAAATAAT 1987
Db 538 TGAATATGTTGGTGGAGTTTGGGCTCGGCTTTTGGTTAGTATGTTCTATATAAAATAAT 597
Qy 1988 TCTCTCTTTTGTGATCTTCCAAATATGATTAATTTTATGTAAGTAAGCAACTTTT 2047
Db 598 TCTCTCTTTTGTGATCTTCCAAATATGATTAATTTTATGTAAGTAAGCAACTTTT 657
Qy 2048 TTAGTAGTGCCCACTTATAGCACAAAAACCTATATCAATTTTCTAATAGTCTTCAAAATC 2107
Db 658 TTAGTAGTGCCCACTTATAGCACAAAAACCTATATCAATTTTCTAATAGTCTTCAAAATC 717
Qy 2108 CACATCTATTTTATAGCCATTTCTTCAAAATGGCAAAATCAGGAAATTTAATACAT 2167
Db 718 CACATCTATTTTATAGCCATTTCTTCAAAATGGCAAAATCAGGAAATTTAATACAT 777
Qy 2168 CTTGCCATAACATATCTAGTGCAAAATGTTAACTAGATTGCTCAATATTAGCAAACTTCT 2227
Db 778 CTTGCCATAACATATCTAGTGCAAAATGTTAACTAGATTGCTCAATATTAGCAAACTTCT 837
Qy 2228 TTGTGAAGATTCATTAATATCTACATGATACATTTTATAGAGTTTCATCAATATGTC 2287
Db 838 TTGTGAAGATTCATTAATATCTACATGATACATTTTATAGAGTTTCATCAATATGTC 897
Qy 2288 CTCATTTAGCACTCTCATTTTAGGAACTTGAATTAACCGCTTAAATAGAGCAAGTG 2347
Db 898 CTCATTTAGCACTCTCATTTTAGGAACTTGAATTAACCGCTTAAATAGAGCAAGTG 956

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```

RESULT 2
CC431905
LOCUS
DEFINITION
PUBF01912D ZM.0.6.1.0.KB Zea mays genomic clone ZMBTA240014,
genomic survey sequence.
ACCESSION
CC431905
VERSION
CC431905.1 GI:30927433
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

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clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 704)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reinick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy Whitelaw
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES
Location/Qualifiers
source
1..704
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBTA240014"
/clone_1lb="ZM 0.6.1.0.KB"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"
ORIGIN
Query Match 25.1%; Score 626.8; DB 8; Length 704;
Best Local Similarity 95.2%; Pred. No. 2.9e-136;
Matches 568; Conservative 0; Mismatches 32; Indels 2; Gaps 2;
Qy 962 GTCCAGGGTCAACAGAGGGGCAAGATCGAGTGTGCGAGTGTCTCCATGGAAGGGA 1021
Db 1 GTCCAGGGTCAACAGAGGGGCAAGATCAATGTGCGAGTGTCTCCATGGAAGGGA 60
Qy 1022 AACTTCGTGAGCAATTCAGATTTCTATATGTGACCGGGTCAGGGAATGGGCGCATG 1081
Db 61 AACTTCGTGAGCAATTCAGATTTCTATATGTGACCGGGTCAGGGAATGGGCGCATG 120
Qy 1082 GGGTTGGTACCTTCTGGTGACATCATGTGTGTGATCGATGTCAAGGAGCATTAGGG 1141
Db 121 GGGTTGGTACCTTCTGGTGACATCATGTGTGTGATCGATGTCAAGGAGCATTAGGG 180
Qy 1142 TTCAGAGTCAGCGATGACGGCATGTGGGACTTGTGTCAACATGGTTCGATCACTAG 1201
Db 181 TTCAGCGTCAGTGTGCGGGCATGTGGGACTGTGTCAACATGGTTCGATCACTAG 240
Qy 1202 GGACATAGAGCTCTATGAAGTTTCAACACTTCTCCACACTCTAGGGATCATGGTGACA 1261
Db 241 GGACATAGAGCTCTATGAAGTTTCAACACTTCTCCACACTCTAGGGATCATGGTGACA 300
Qy 1262 AGGTGGGNGACGGGGCTCTCTAGTGAAGGTGGAATGCACTTCTGTCACTGGGAATA 1321
Db 301 AGGTGGGNGACGGGGCTCTCTAGTGAAGGTGGAATGCACTTCTGTCACTGGGAATA 360
Qy 1322 GTGGCGGCATCGCTTCTTAATGAATAAAGGTGCTTGGGTGGTGGGAAGTCAATATGAG 1381
Db 361 GTGGCGGCATCGCTTCTAGTGAAGTGAAGGTGCTTGGGTGGTGGG-AGTGAATATGAG 419
Qy 1382 GGAATAGTGTGGTGGGGATGTTCTTTTATAGGGGACACCATTTGATTAATGGAGAC 1441
Db 420 GGAATAGTGTGGTGGGGATGTTCTTTTATAGGGGACACCATTTGATTAATGGAGAC 479
Qy 1442 AATGACAAAGGTGGTGGCAGCATGTTTAAAGCTCGAATGTCTGATAGGGGTCTCAAGGT 1501
Db 480 AATGACAGAGGGTGGTGGCAGCATTTTAAAGCTCGAATGTCTGATAGGGGTCTCAAGGT 539
Qy 1502 TAAGATACAGGCATCAGGAGGAAAGCAGCGGATTAATTTCTTACTCCAGTTGGGG 1561
Db 540 TAATGATCAGGCATCAGGAGGAAAGCAGCGGATTAATTTCTTACTCTAGTTGGGG 599
Qy 1562 GTGATGGGGAAGAGGTAGTGTCAAGCAAGGAGGCGAGTTCAGCGCAGAGATGCTG 1621

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Db 924 TGTGGAGTTGGGCTCCGCTTTGGTAGTATGTTGTATATAAATAATTTCTCTCTT 865  
Qy 1997 TTGTCACTTCAATATATGACTTAATAATTTTATGTAGCAATGCCAATTTTATAGTAGT 2056  
Db 864 TTGTCACTTCAATATATGACTTAATAATTTTATGTAGCAATGCCAATTTTATAGTAGT 805  
Qy 2057 TGGCACTATAGCAAAACTATATCCATTTTCTAATAGTCTTTGAATCCACATTTCTA 2116  
Db 804 TGGCACTATAGCAAAACTATATCCATTTTCTAATAGTCTTTGAATCCACATTTCTA 745  
Qy 2117 TTTTATAGCCATTTCTCAAAATTTGGCAAAACTAGGAAATTTAATACATTTCTGCCATA 2176  
Db 744 TTTTATAGCCATTTCTCAAAATTTGGCAAAACTAGGAAATTTAATACATTTCTGCCATA 685  
Qy 2177 ACATATTTCTAGTCAAAATTTAACTAGATTTGCTCAATATAGCAAACTTTCTTTGAAGA 2236  
Db 684 ACATATTTCTAGTCAAAATTTAACTAGATTTGCTCAATATAGCAAACTTTCTTTGAAGA 625  
Qy 2237 TTCAATTAATATGCTACATGCAATCTTTTATAGAAATTTCAATATAGCTCTATAGC 2296  
Db 624 TTCAATTAATATGCTACATGCAATCTTTTATAGAAATTTCAATATAGCTCTATATC 565  
Qy 2297 ATACTTCAATTTTAGCACTTGAATTAACCGCTTAAATAGAGCAAGTACGATCCA 2356  
Db 564 ATACTTCAATTTTAGCACTTGAATTAACCGCTTAAATAGAGCAAGTACGATCCA 505  
Qy 2357 -TTTAAAGTCAATTTCTTAATTTCTTACTTCTCTATCTTTGGTGGCTTAATATATGT 2415  
Db 504 CTTTAAAGTCAATTTCTTAATTTCTTACTTCTCTATCTTTGGTGGCTTAATATATGT 445  
Qy 2416 GTGGTGGTTCGAATGATGTTCTTACACCACTACACCACTTGGACATATATATGGAAA 2475  
Db 444 GTGGTGGTTCGAATGATGTTCTTACACCACTACACCACTTGGACATATATATGGAAA 385  
Qy 2476 ATAGCTTACAGTCTAGA 2493  
Db 384 ATAGCTTACAGTCTAGA 367

## RESULT 5

BZ407849 555 bp DNA linear GSS 04-DEC-2002  
LOCUS OGAC134TM.ZM.0.7.1.5\_KB\_Zea\_mays\_genomic\_clone\_ZM8Ma0029E19,  
DEFINITION genomic survey sequence.

## ACCESSION

BZ407849

## VERSION

BZ407849.1 GI:26037521

## KEYWORDS

GSS.

## SOURCE

Zea mays

## ORGANISM

Zea mays

## REFERENCE

1 (bases 1 to 555)

## AUTHORS

Whitehead, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

## TITLE

Unpublished (2002)

## JOURNAL

Other GSSs: OGAC134TC

## COMMENT

Contact: Cathy Whitelaw

## TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

## Tel:

301-838-5843

## Fax:

301-838-0208

## Email:

whitelaw@tigr.org

## Seq primer:

TR

## Class:

Sheared ends.

## FEATURES

Location/Qualifiers

1..555

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

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Best Local Similarity 98.1%; Pred. No. 5.2e-78;  
Matches 415; Conservative 0; Mismatches 5; Indels 3; Gaps 3;  
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/clone\_lib="ZM.0.7.1.5\_KB"  
/notes="Vector: pBC8K; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

## ORIGIN

Qy 1 AAGCTTTTCGGTGAATGAAGCACTCTGTAATATCTTAACAGCATGCTGAAACAAATAGTTA 60  
Db 135 AAGCTTTTCGGTGAATGAAGCACTCTGTAATATCTTAACAGCATGCTGAAACAAATAGTTA 194  
Qy 61 GCTGTGTTTTTGGAGCACTTCGGAGATGAAGGCCCAACACATCCCATGATCAAGTC 120  
Db 195 GCTGTGTTTTTGGAGCACTTCGGAGATGAAGGCCCAACACATCCCATGATCAAGTC 254  
Qy 121 CCATGACTTGCAGCAAAAGCAAAATTTTATC-AAAATTTCTCATAAACACTTGAAAAACAT 179  
Db 255 CCATGACTTGCAGCAAAAGCAAAATTTTATC-AAAATTTCTCATAAACACTTGAAAAACAT 314  
Qy 180 TTCTCTTTTGGAAAGGTGTAGAGCACTAGCAACTGTCTACTATAAAGGTTCCCAATTTTC 239  
Db 315 TTCTCTTTTGGAAAGGTGTAGAGCACTAGCAACTGTCTACTATAAAGGTTCCCAATTTTC 374  
Qy 240 TGGGTATTAACAAATGCGCATGGTAAATAACAAGGAAATCTCTACTAAGAGCAGTAAATTTG 299  
Db 375 TGGGTATTAACAAATGCGCATGGTAAATAACAAGGAAATCTCTACTAAGAGCAGTAAATTTG 434  
Qy 300 GCTTAAACAAATAGTAGAGCACTTTTAAATGTAAATAGGAAATAGGAGCATGCTACTTGTGT 359  
Db 435 GCTTAAACAAATAGTAGAGCACTTTTAAATGTAAATAGGAAATAGGAGCATGCTACTTGTGT 493  
Qy 360 CTTTCAGGTTTTGTATGTCCTCAAAAGTGTGCCCCCTGGGGCAGTTGCAACACTCAAAA 419  
Db 494 CTTTCAGGTTTTGTATGTCCTCAAAAGTGTGCCCCCTGGGGCAGTTGCAACACTCAAAA 552  
Qy 420 TCT 422  
Db 553 TCT 555

## RESULT 6

BZ407846/c

## LOCUS

BZ407846

## DEFINITION

genomic survey sequence.

## ACCESSION

BZ407846

## VERSION

BZ407846.1 GI:26037516

## KEYWORDS

GSS.

## SOURCE

Zea mays

## ORGANISM

Zea mays

## REFERENCE

1 (bases 1 to 578)

## AUTHORS

Whitehead, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

## TITLE

Unpublished (2002)

## JOURNAL

Other GSSs: OGAC134TM

## COMMENT

Contact: Cathy Whitelaw

## TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

## Tel:

301-838-5843

## Fax:

301-838-0208

## Email:

whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..578

source

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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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methylation filtered genomic DNA library"
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## ORIGIN

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Best Local Similarity 98.2%; Pred. No. 2.3e-72;
Matches 380; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Qy 1 AAGCTTTCCGTTGATGAGCAGCCTGTATATCTTAACAGCATGCTGAAACAAATAGTTA 60
Db 386 AAGCTTTCCGTTGATGAGCAGCCTGTATATCTTAACAGCATGCTGAAACAAATAGTTA 327
Qy 61 GCTGTGTTTTCAGGACCTTCGAGATGAGGCCCCCAACACATCCCATGCATCAAGTC 120
Db 326 GCTGTGTTTTCAGGACCTTCGAGATGAGGCCCCCAACACATCCCATGCATCAAGTC 267
Qy 121 CCCATGACTGCAAAAGCAAAATTTTATC-AAAATTTCTCATAAACACATTTGAAAACAT 179
Db 266 CCCATGACTGCAAAAGCAAAATTTTATCAAAATTTCTCATAAACACATTTGAAAACAT 207
Qy 180 TTCTCTTTTGAAGTGTAGACACTAGCACTGCTACTAAAGGTTCCCAATTTTC 239
Db 206 TTCTCTTTTGAAGTGTAGACACTAGCACTGCTACTAAAGGTTCCCAATTTTC 147
Qy 240 TGGGTATAACAATCGCATGGTAAATAACAAGGAAATCTACTAAGAGCAGTAAATTTG 299
Db 146 TGGGTATAACAATCGCATGGTAAATAACAAGGAAATCTACTAAGAGCAGTAAATTTG 87
Qy 300 GCTAAACAAATAGTACCATTTTAATGTAATAGGCAATAGGAGTCATCACTTGTGTT 359
Db 86 GCTAAACAAATAGTACCATTTTAATGTAATAGGCAATAGGAGTCATCACTTGTGTT 28
Qy 360 CTTTCAGGGTTTTGATGTCTCTCAAAAG 386
Db 27 CTTTCAGGGTTTTGAGTCTCTAAAG 1
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## RESULT 7

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CL984849/c
LOCUS      ZMMBHD0002122.f ZMMBHD Zea mays genomic clone ZMMBHD0002122 5',
DEFINITION genomic survey sequence.
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ACCESSION  CL984849
VERSION    CL984849.1
KEYWORDS   GSS.
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## SOURCE

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1114)

Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and  
Bennetzen,J.

ZMMBH sequences

Unpublished (2004)

Contact: Jeff Bennetzen

Bennetzen Lab

The University of Georgia

Department of Genetics, C426a Life Sciences Building, Athens, GA

30602, USA

Tel: 706-542-3698

Fax: 706-583-0972

Email: maize@uga.edu

Plate: 0002 row: j column: 22

Class: BAC ends.

Location/Qualifiers

## FEATURES

source

1..1114

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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBHD0002122"
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/dev_stage="6-8 weeks"
/lab_host="DH10B"
/clone_lib="ZMMBHD"
/notes="Vector: TOPOcr4; Site_1: EcoRI; Site_2: EcoRI"
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## ORIGIN

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Query Match      13.2%; Score 328.6; DB 9; Length 1114;
Best Local Similarity 64.8%; Pred. No. 4.2e-66;
Matches 627; Conservative 0; Mismatches 329; Indels 11; Gaps 9;

Qy 266 ACACAAAGGAAATCTCTAAGAGCAGTAATTTGGCTTAAACAATAGTAGACATTTTAAT 325
Db 1005 ACCCTTAAGTAGTACTAATAGGAGTAGTAATTTGGCCAAACAAATANTGACAT-TTTAT 947
Qy 326 GTAATAGGGAATAGGAGCATGCAATATCTTGTGTTCTTTCAAGGTTTTGATGTCCTCAAA 385
Db 946 GCATAGGGTGATACGAGGATAGAAATGTTTCTTCTCGGGTTTCGAGGTCCTCAAGA 887
Qy 386 GTGTGCCCCCTGGGGCAGTTGCAACACTCAAAATCTACTCGTATACATA-AAGAACAT 444
Db 886 GTGGGGCCCTC-GAGTAGTTGCAACATTTATGATCTACTCGTTCATNTAATNAACAT 828
Qy 445 GGGCACAATAATGAAGAAACATCTCAATTTATGAAAAA---AGGTTCAATGTCCTATAA 501
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Qy 1099 GTGCACATCATGTTGCTGTATCGATGTCAGGGAGCAATTAGGGGTTCAAGGATGAGCGATG 1158
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The University of Georgia  
Department of Genetics, C426a Life Sciences Building, Athens, GA  
30602, USA  
Tel: 706-542-3698  
Fax: 706-583-0972  
Email: maize@uga.edu  
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# FEATURES

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Db 968 -CAACATAATGAACA-TTAAATGCAATGGGTGATACGAGGATAGATGTTTCTCTCT 911

Qy 362 TTACGGTTTTCATGCTCTCAAAAGTGTGCCCTCGGGCAGTTGCAACTCAAAATC 421  
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ACCESSION CL996043  
VERSION CL996043.1 GI:52565370  
KEYWORDS GSS.

SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 1035)  
AUTHORS Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and Bennetzen,J.

TITLE ZMMBF sequences  
JOURNAL Unpublished (2004)  
COMMENT Contact: Jeff Bennetzen  
Bennetzen Lab  
The University of Georgia  
Department of Genetics, C426a Life Sciences Building, Athens, GA  
30602, USA  
Tel: 706-542-3698  
Fax: 706-583-0972  
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Matches 627; Conservative 0; Mismatches 349; Indels 15; Gaps 11;

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 VERSION CG171826.1 GI:34062624  
 KEYWORDS GSS.

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 AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennettzen,J.  
 TITLE Maize Genomics Consortium  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
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Qy 209 CAAACAATAGTAACA- TTTAATGCAATGGGTGATACAGGATAGAAATGTTTCTCT 267
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genomic survey sequence.
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CG067437
VERSION
CG067437.1 GI:33939617
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays

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# REFERENCE

1 (bases 1 to 788)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Bennett, J., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and Maiz Genetics Consortium  
Unpublished (2003)  
Other GSSs: FUIR86TD  
Contact: Cathy Whitelaw  
TIGR

# TITLE

Maiz Genetics Consortium  
Unpublished (2003)  
Other GSSs: FUIR86TD  
Contact: Cathy Whitelaw  
TIGR

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Best Local Similarity 64.6%; Pred. No. 8e-38;
Matches 453; Conservative 0; Mismatches 233; Indels 15; Gaps 9;

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Db 532 TTA-AGAAAGTGGGTTATTTATTTTAAATTTGTCATAGACTGCATGGTTTAAAAAGTATAT 590
Qy 647 TTTGGGTCCTCTAGTTGGAACCTAGCTCAGATTTGCTGTTGATTTTCCATAAAAGTCCAGGTT 706
Db 591 TTGATGTCCTCTAGTTAGAACCAAGATTCGGACTGTGTTGATTTTAAATTAAGCCAGAGGT 650

```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:52:07 ; Search time 1329 Seconds  
(without alignments)  
11367.636 Million cell updates/sec

Title: US-10-089-612-2  
Perfect score: 2493  
Sequence: 1 aagctttccggatgaag.....aatagcttcacagtctaga 2493

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11210502

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCU\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCU\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73.4	2.9	602	18	US-10-425-115-24619 Sequence 24619, A
2	72.8	2.9	438	18	US-10-425-115-69828 Sequence 69828, A
3	72	2.9	495	18	US-10-425-115-93280 Sequence 93280, A
4	71.6	2.9	812	18	US-10-425-115-1000 Sequence 1000, A
5	62.4	2.5	2096	17	US-10-425-114-1206 Sequence 1206, A
6	62.4	2.5	2096	18	US-10-425-115-59907 Sequence 59907, A
7	62	2.5	8056	18	US-10-425-115-386 Sequence 386, App
8	59	2.4	493	18	US-10-425-115-45669 Sequence 45669, A
9	58.8	2.4	8056	18	US-10-473-126-240 Sequence 240, App
10	58.4	2.3	308	18	US-10-425-115-81221 Sequence 81221, A
11	56.4	2.3	1137	17	US-10-425-114-3317 Sequence 3317, A

C	12	56.4	2.3	1489	18	US-10-425-115-134984 Sequence 134984, A
	13	55.4	2.2	398	18	US-10-425-115-85377 Sequence 85377, A
	14	53.8	2.2	367378	16	US-10-312-841-1 Sequence 1, Appl
C	15	53.2	2.1	6863	17	US-10-221-714A-339 Sequence 339, App
C	16	52	2.1	12669	17	US-10-221-613-412 Sequence 412, App
	17	51.8	2.1	1157	18	US-10-425-115-161110 Sequence 161110, App
	18	51.8	2.1	5252	18	US-10-311-455-1108 Sequence 1108, App
C	19	51.8	2.1	9810	15	US-10-311-455-399 Sequence 399, App
	20	51.4	2.1	12142	15	US-10-311-455-1646 Sequence 1646, App
	21	51	2.0	15548	15	US-10-311-455-2128 Sequence 2128, App
	22	50.8	2.0	3252	13	US-10-027-632-113786 Sequence 113786, App
	23	50.8	2.0	3252	13	US-10-027-632-113787 Sequence 113787, App
	24	50.8	2.0	3252	13	US-10-027-632-113788 Sequence 113788, App
	25	50.8	2.0	3252	17	US-10-027-632-113786 Sequence 113786, App
	26	50.8	2.0	3252	17	US-10-027-632-113787 Sequence 113787, App
	27	50.8	2.0	3252	17	US-10-027-632-113788 Sequence 113788, App
C	28	50.6	2.0	7924	15	US-10-311-455-2112 Sequence 2112, App
C	29	50.6	2.0	7924	17	US-10-257-166-152 Sequence 152, App
C	30	50.4	2.0	13377	15	US-10-311-455-1436 Sequence 1436, App
C	31	50.4	2.0	13377	17	US-10-221-714A-198 Sequence 198, App
C	32	50.2	2.0	5488	15	US-10-311-455-1429 Sequence 1429, App
C	33	50.2	2.0	337344	18	US-10-388-838-58 Sequence 58, Appl
C	34	50	2.0	34688	18	US-10-433-793-90 Sequence 90, Appl
	35	49.8	2.0	7442	17	US-10-221-714A-409 Sequence 409, App
	36	49.6	2.0	113515	15	US-10-311-455-2148 Sequence 2148, App
	37	49.4	2.0	843	13	US-10-027-632-7034 Sequence 7034, App
	38	49.4	2.0	843	17	US-10-027-632-7034 Sequence 7034, App
C	39	49.4	2.0	367378	16	US-10-312-841-2 Sequence 2, Appl
	40	49.2	2.0	671	14	US-10-184-644-346 Sequence 346, App
	41	49.2	2.0	671	14	US-10-184-634-346 Sequence 346, App
C	42	48.8	2.0	2000	9	US-09-938-842A-4957 Sequence 4957, App
C	43	48.8	2.0	2000	11	US-09-938-842A-4957 Sequence 4957, App
C	44	48.8	2.0	4045	17	US-10-221-714A-466 Sequence 466, App
	45	48.8	2.0	5238	15	US-10-311-455-731 Sequence 731, App

## ALIGNMENTS

### RESULT 1

US-10-425-115-24619  
; Sequence 24619, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 24619  
; LENGTH: 602  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_12245C.1  
; US-10-425-115-24619

Query Match	2.9%	Score	73.4	DB	18	Length	602
Best Local Similarity	83.8%	Pred. No.	4.3e-06				
Matches	83	Conservative	0	Mismatches	16	Indels	0
Oy	1	AAGCTTTCCGGTGAAGCAGCTGTAATCTTAAACAGCATCTGTAACAAATAGTTA	60				
Db	204	ANGCTTTCTGTAAGAGCTTCTATATATTTAATAGTATCTGTAAGCAATAGTTA	263				
Oy	61	GCTGTGTTTTCGAGCCTTCGGAAGATGAAGGCCCA	99				
Db	264	CCCTGTGTTTTCGAGCCTTCGGAAGATGAAGGCCCA	302				

[illegible]

Qy	294	AAATTGGCTAAACAATAGTGCATTT	321
Db	94	AAATTAGCAGAAACAGTAATGAACATTT	67
RESULT 4			
US-10-425-115-1000/c			
; Sequence 1000, Application US/10425115			
; Publication No. US20040214272A1			
; GENERAL INFORMATION:			
; APPLICANT: La Rosa, Thomas J.			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; TITLE OF INVENTION: Plants			
; FILE REFERENCES: 38-21(53222)B			
; CURRENT APPLICATION NUMBER: US/10/425.115			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 369326			
; SEQ ID NO 1000			
; LENGTH: 812			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURES:			
; OTHER INFORMATION: Clone ID: MRT4577_100912C.1			
US-10-425-115-1000			
Query Match 2.9%; Score 71.6; DB 18; Length 812;			
Best Local Similarity 81.4%; Pred. No. 1.3e-05;			
Matches 83; Conservative 0; Mismatches 19; Indels 0; Gaps 0;			
Qy	1	AAGCTTTCCGGTGTGATGAGCACCCTGTAATACTTAACGACGATCTGAAACAAATAGTTA	60
Db	399	AAGCTTTTCTTATGACGAGCTCATGTAATATTTAGTAGTAGTATGTAACAAACAATAGTTA	340
Qy	61	GCTGTGTTTTTGGAGCACCTTCGGAAGATGAAGCCCCCAACA	102
Db	339	GTCATGTTTTTGGAGCACCTTCGAAAGAGTAAAGCCCCCAACA	298
RESULT 5			
US-10-425-114-1206/c			
; Sequence 1206, Application US/10425114			
; Publication No. US20040034886A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Jingdong			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Screen, Steven E.			
; APPLICANT: Tabaska, Jack E.			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement			
; FILE REFERENCES: 38-21(53113)B			
; CURRENT APPLICATION NUMBER: US/10/425.114			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 73128			
; SEQ ID NO 1206			
; LENGTH: 2096			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURES:			
; OTHER INFORMATION: Clone ID: 700104722_FLI			
US-10-425-114-1206			
Query Match 2.5%; Score 62.4; DB 17; Length 2096;			
Best Local Similarity 68.2%; Pred. No. 0.0025;			
Matches 101; Conservative 0; Mismatches 46; Indels 1; Gaps 1;			
Qy	1	AAGCTTTTCCGGTGTGATGAGCACCCTGTAATACTTAACGACGATCTGAAACAAATAGTTA	60
Db	1769	AGTTTTTCTAGTAAGCAGACTCTGTAACTTCTTAATACATACCTGAAATAAATAGTTA	1710

Oy 61 GCTGTGTTTTCAGGACCTTCGGAAGATGAAGGCCGCCCAACACATCCCATCAAGTC 120  
Db 1709 ACCGTGTTTT-AAGACCTTCAGAGAGAGAGGCCGCCCAAGACCACTGAACCTGATGAC 1651  
Oy 121 CCATGACCTTCGAAAAGCAATTTTA 148  
Db 1650 ACAACATTAATGAAGACATCTCATGCTA 1623

## RESULT 6

US-10-425-115-59907/c  
; Sequence 59907, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 59907  
; LENGTH: 2096  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_154633C.1  
US-10-425-115-59907

Query Match 2.5%; Score 62.4; DB 18; Length 2096;  
Best Local Similarity 68.2%; Pred. No. 0.0025;  
Matches 101; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

Oy 1 AGCGTTTCGGTGATGAAGACCTGTAATCTTAACGACATGCTGAACCAATAGTTA 60  
Db 1769 AAGTTTTTCTAGTACGAGCTCTGTGTAATCTTAATACATCTGAATAATAGTTA 1710  
Oy 61 GCTGTGTTTTCAGGACCTTCGGAAGATGAAGGCCGCCCAACACATCCCATCAAGTC 120  
Db 1709 ACCGTGTTTT-AAGACCTTCAGAGAGAGAGGCCGCCCAAGACCACTGAACCTGATGAC 1651  
Oy 121 CCATGACCTTCGAAAAGCAATTTTA 148  
Db 1650 ACAACATTAATGAAGACATCTCATGCTA 1623

## RESULT 7

US-10-473-126-386/c  
; Sequence 386, Application US/10473126  
; Publication No. US20040214973A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell  
; FILE OF INVENTION: proliferative disorders  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/473,126  
; CURRENT FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 1258  
; SEQ ID NO 386  
; LENGTH: 8056  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-473-126-386

Query Match 2.5%; Score 62; DB 18; Length 8056;  
Best Local Similarity 45.5%; Pred. No. 0.0062;  
Matches 221; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

Oy 1852 AATTGAAGTGAATTTTAAATCAATCAATGACCTCCAAATCTCTCAAAATTTACCAA 1911  
Db 2361 AATTATATTTAAATAATTTAAATAATTTTAAATACAAAATTTAAATAATTTATTTAA 2302  
Oy 1912 ATATGAATATTTAGATGAATATGTTGGTGGAGTTTGGGCTCCGCTTTGGTTAGTATCT 1971  
Db 2301 AAATAAATAATTTAAATAATTTTAAATTTTAAATTTTAAATAATTTAAATAAAT 2242  
Oy 1972 TTGTATAAAATAAATTTCTCTCTCTTTTGTCTCACTTCCAAATTTGACTTAAATTTTATGTA 2031  
Db 2241 TTTTATTAATAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2182  
Oy 2032 GCAATGCCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2091  
Db 2181 ATAAATAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2122  
Oy 2092 AATAGTCTTGAATAATCCACATTTCTATTTTAAATTTTAAATTTTAAATTTTAAATTT 2151  
Db 2121 AATATATTAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2062  
Oy 2152 GAAATTTAATACATTTCTGCCATACATATTTCTAGTGCATATGTTAACTAGATGCTCA 2211  
Db 2061 TTTTAAATAATTAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2002  
Oy 2212 ATATTAGCAAACTTCTTTTCTAGATTTCAATTAATTTGCTACATTTGCTATGCTATGTA 2271  
Db 2001 AATTTTAAATAATAATTTAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1942  
Oy 2272 AGTTTCATCAATATGCTCTCATTTAGCATCTCTATTTAGGAATCTGATTAATAACCGCTT 2331  
Db 1941 ATATTATTAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1882  
Oy 2332 AAAATA 2337  
Db 1881 AAAATA 1876

## RESULT 8

US-10-425-115-45669  
; Sequence 45669, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 45669  
; LENGTH: 493  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_141656C.1  
US-10-425-115-45669

Query Match 2.4%; Score 59; DB 18; Length 493;  
Best Local Similarity 78.0%; Pred. No. 0.0068;  
Matches 71; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Oy 23 CCTGTATATTTAACAGCATGCTGAAAACAAATAGTTAGCTGTGTTTTGAGGACCTTGG 82  
Db 370 CCTGTATATGCTATATCATCTGAAAACAAATAGTTAGTACATTTTGGACCTTGG 429  
Oy 83 GAAGATGAAGGCCGCCCAACACATCTCCATGCA 113  
Db 430 GAAGAGGAGGCCCTCAACACATTAATCTTGA 460

```
RESULT 9
US-10-473-126-240/c
; Sequence 240, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 240
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-240

Query Match      2.4%; Score 58.8; DB 18; Length 8056;
Best Local Similarity 45.1%; Pred. No. 0.032;
Matches 219; Conservative 0; Mismatches 267; Indels 0; Gaps 0;

QY 1852 AATTTAAGTTCGAATTTTAAATCCAAATCAATGACCTCCAAATCTCTCCAAATATACCAAA 1911
      |||||
DB 2361 AATATATTTAAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTAATTAATTTTAA 2302

QY 1912 ATATAGAAATATTAGATGAATATGTTGGTGGAGTTTGGGCTCCGCTTTGGTTAGTATGT 1971
      |||||
DB 2301 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2242

QY 1972 TTGTATAAAATAAATTTCTCTCTCTTTTGTGACCTTCCAAATATGACTTAATTTTATGTA 2031
      |||||
DB 2241 TTTTATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2182

QY 2032 GCAATGCCAACTTTTGTAGTAGTGCCACTTATAGCACAAAACATATATCCATTTCTT 2091
      |||||
DB 2181 ATAAAAATATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 2122

QY 2092 AATAGTCTTGAATCCACATCTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 2151
      |||||
DB 2121 AATATATTAATTAATTTATATATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2062

QY 2152 GAAATTTAATACATCTTCCCAATACATATTTCTAGTGCATATGTTAACTAGATGCTCA 2211
      |||||
DB 2061 TTTTAAAAATAAAAAATATTTAAAAAATATTTTATTTTAAATATATTTTAAATTTTATTT 2002

QY 2212 ATATTAGCAACTCTTTTGTAGATTCATTAATATTTGCTACATTCATATCTTTTATAGA 2271
      |||||
DB 2001 AATTTTAAATAAATAATTAATTAATTTATTTTATTTTAAATTTATTTTATTTTATTTTAT 1942

QY 2272 AGTTCAATCAATAGCTTCATTTAGCATCTTCATTTTATAGCACTTGATTAACCGCCTT 2331
      |||||
DB 1941 ATATTATTAATTAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1882

QY 2332 AAAATA 2337
      |||||
DB 1881 AAAATA 1876

RESULT 10
US-10-425-115-81221/c
; Sequence 81221, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3317
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700259576_FLI
US-10-425-114-3317

Query Match      2.3%; Score 56.4; DB 17; Length 1137;
Best Local Similarity 80.5%; Pred. No. 0.04;
Matches 66; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 23 CCTGTAACTACTTAACAGCATGCTGAAACAAATAGTTAGCTGTGTTTTGAGGACCTTCG 82
      |||||
DB 778 CCTGTAACTACTACTATTATGCTAGAACAAATGTTAGTCATGTTTTGAGGACCTTAG 719

QY 83 GAAGATGAAGGCCCCCAACACA 104
      |||||
DB 718 AAAGAGGAAGGCCCCCAACAAA 697

RESULT 12
US-10-425-115-134984/c
; Sequence 134984, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3317
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700259576_FLI
US-10-425-114-3317

Query Match      2.3%; Score 56.4; DB 17; Length 1137;
Best Local Similarity 80.5%; Pred. No. 0.04;
Matches 66; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 23 CCTGTAACTACTTAACAGCATGCTGAAACAAATAGTTAGCTGTGTTTTGAGGACCTTCG 82
      |||||
DB 778 CCTGTAACTACTACTATTATGCTAGAACAAATGTTAGTCATGTTTTGAGGACCTTAG 719

QY 83 GAAGATGAAGGCCCCCAACACA 104
      |||||
DB 718 AAAGAGGAAGGCCCCCAACAAA 697

RESULT 11
US-10-425-114-3317/c
; Sequence 3317, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3317
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700259576_FLI
US-10-425-114-3317

Query Match      2.3%; Score 58.4; DB 18; Length 308;
Best Local Similarity 85.5%; Pred. No. 0.0072;
Matches 65; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 27 TAATACTTAACAGCATGCTGAAACAAATAGTTAGCTGTGTTTTGAGGACCTTCGGAAG 86
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DB 308 TAATACTTCAATATATGCTGAAACAAACAGATGTTAGCGTGTATTAAAGGACCTTCGAAAA 249

QY 87 ATGAAGGCCCCCAACA 102
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DB 248 ATGAAGGCCCCCAACA 233
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Qy	1840	TTCTCCANTCCCAATTTAGTTGAATTTTAAATCAATCAATGACTCCAAATCTCTCC	1899
Db	6224	TTCAAAATTTCCAAATCAACTTAACAAACAAATATAAACCTCCCAACAAATAATAAAC	6165
Qy	1900	AAATTTACCAAAATATAGAAATATTTAGATGAATATGTTGGTGGAGTTTGGGCTCCGCTTT	1959
Db	6164	CAAAACACATTAAACGAAAAATTTATATTTTACTAAATAATAAATACTATATTTCTTCATATT	6105
Qy	1960	TGGTTAGTATGTTGTATATAAATAATTTCTCTCTCTCTTTGTGCACTTCCAAATATGACTTA	2019
Db	6104	TTTTCAAAATATATCAACCATATATATCAATAACTTTCTTACTTAAACCTACTTTA	6045
Qy	2020	AAATTTTATAGCAATGCCAACTTTTTTTAGTAGTGTGCCACTTATAGCACAAAACTA	2079
Db	6044	AAATAATTACAAAAAAATTTTAATAATTTTCTATCAAACTCCAACTTTTAAAAAAAATCAA	5985
Qy	2080	TATCCATTTTCTAATAGTCTTGAATCCCACTCTATTTTGTAGCCATCTCTCAAAATTG	2139
Db	5984	AAATATATAAATTTATATATACATTCACATTCATATATTTCCAAACGCTCTTATACACTAAT	5925
Qy	2140	GCACAAACTAGGAATTTTAATACATCT	2169
Db	5924	ATTCATTTTATAAACAATCAATCGTCT	5895

Search completed: April 9, 2005, 10:52:17  
Job time : 1337 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 02:16:11 : Search time 432 Seconds  
(without alignments)  
9442.680 Million cell updates/sec

Title: US-10-089-612-2

Perfect score: 2493

Sequence: 1 agctttccggtgatgaag.....aaatagcttcacagctctaga 2493

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	74	3.0	7218	1	US-08-232-463-14
C 2	56	2.2	1141	4	US-09-806-708B-22
C 3	55.2	2.2	30820	4	US-09-949-016-17145
C 4	51.2	2.1	1664976	4	US-08-916-421B-1
C 5	51.2	2.1	1664976	4	US-09-692-570-1
C 6	48.2	1.9	601	4	US-09-949-016-30530
C 7	48.2	1.9	601	4	US-09-949-016-30531
C 8	48.2	1.9	601	4	US-09-949-016-37149
C 9	48.2	1.9	601	4	US-09-949-016-37150
C 10	48.2	1.9	601	4	US-09-949-016-37163
C 11	48.2	1.9	601	4	US-09-949-016-37164
C 12	48.2	1.9	601	4	US-09-949-016-145867
C 13	48.2	1.9	601	4	US-09-949-016-145868
C 14	48.2	1.9	601	4	US-09-949-016-146135
C 15	48.2	1.9	601	4	US-09-949-016-146136
C 16	48.2	1.9	601	4	US-09-949-016-146403
C 17	48.2	1.9	601	4	US-09-949-016-146404
C 18	48.2	1.9	205044	4	US-09-949-016-15851
C 19	48.2	1.9	205044	4	US-09-949-016-15852
C 20	48.2	1.9	205044	4	US-09-949-016-15853
C 21	48.2	1.9	223471	4	US-09-949-016-12387
C 22	48.2	1.9	223471	4	US-09-949-016-12724
C 23	48.2	1.9	223471	4	US-09-949-016-12725
C 24	48	1.9	251682	4	US-09-949-016-11793
C 25	48	1.9	251682	4	US-09-949-016-11796
C 26	47.6	1.9	19124	2	US-08-487-836B-13
C 27	46.6	1.9	2121	4	US-09-248-796A-4904

C 28	46.4	1.9	67755	4	US-09-949-016-13703	Sequence 13703, A
C 29	46.2	1.9	601	4	US-09-949-016-54020	Sequence 54020, A
C 30	46.2	1.9	601	4	US-09-949-016-108654	Sequence 108654, A
C 31	46.2	1.9	1141	4	US-09-806-708B-22	Sequence 22, Appl
C 32	46	1.8	660	1	US-07-991-867B-32	Sequence 32, Appl
C 33	46	1.8	660	1	US-08-107-755A-32	Sequence 32, Appl
C 34	46	1.8	660	2	US-08-544-312-32	Sequence 32, Appl
C 35	46	1.8	660	3	US-09-370-861A-32	Sequence 32, Appl
C 36	46	1.8	1511	1	US-07-991-867B-8	Sequence 8, Appl
C 37	46	1.8	1511	1	US-08-107-755A-8	Sequence 8, Appl
C 38	46	1.8	1511	2	US-08-544-312-8	Sequence 8, Appl
C 39	46	1.8	1511	3	US-09-370-861A-8	Sequence 8, Appl
C 40	46	1.8	4810	3	US-08-852-629-11	Sequence 11, Appl
C 41	46	1.8	4838	3	US-08-852-629-15	Sequence 15, Appl
C 42	45.6	1.8	3848	2	US-08-808-931-14	Sequence 14, Appl
C 43	45.6	1.8	3848	3	US-08-808-323-14	Sequence 14, Appl
C 44	45.6	1.8	3848	3	US-09-050-603A-14	Sequence 14, Appl
C 45	45.6	1.8	3848	3	US-09-102-420B-14	Sequence 14, Appl

## ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-3300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
CLONE: pTZgpt-F18  
US-08-232-463-14

Query Match 3.0%; Score 74; DB 1; Length 7218;

[illegible]

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RESULT 2
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent NO. 6784342
; GENERAL INFORMATION:
; TITLE: The University of British Columbia
; APPLICATION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
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; ORGANISM: Artificial sequence
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US-09-806-708B-22

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Qy	2102	GAATATCCACAT-----TCTATTTTTAGCCATCTCTCAAAATTTGGCACAAAACCTAGGAAAT	2157
Db	528	RWAGTWRRHNNNNNTDTRYVWKKWABRTTTVYDSKCNKAKSMWRGNMRZAKHMKWAAN	469
Qy	2158	TTAATACATCTTTGCCATAACATATCTAGTGCAAAATGTTAACTAGATGTCCTCAATATTA	2217
Db	468	NDAGAMDHVTTWNGNTWMMRWKMMKMMWACRGRAYCENNNNRACVWHRHOMRWMTKX	409
Qy	2218	GCAAACTCTTTTGTGAAGATTCATTAATGCTACATGCTACATCTTTTTTAGAGTTCA	2277
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Qy	2278	TCAATAATGCTCATTAGCATACTTCATTTTAGGAACCTGATTAACACGGCTTTAAATA	2337
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Qy	2338	GAGCAAGTGAOCGGATFCCATTTAAAGGAGTCTTTAAATTTCTTCTACTCTTTGGTG	2397
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Qy	2398	GCTATGTTTATATATGTGCGGTGGTTCGAAATGATGTTCTCTACACCATCACACACCT	2457
Db	231	HNBWRBRABHRSNNMWKCNKYVSWHYHABYBKWABVGCNNNNKDRMAHHWCAT	172
Qy	2458	TGGACATATATAT	2470
Db	171	NNNNNNWYATNCH	159

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RESULT 3
US-09-949-016-17145
/ Sequence 17145, Application US/09949016
/ Patent No. 6812339
/
/ GENERAL INFORMATION:
/
/ APPLICANT: VENTER, J. Craig et al.
/
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/
/ FILE REFERENCE: CLO01307
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/ CURRENT APPLICATION NUMBER: US/09/949,016
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/ CURRENT FILING DATE: 2000-04-14
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/ PRIOR APPLICATION NUMBER: 60/241,755
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/ PRIOR FILING DATE: 2000-10-20
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/ PRIOR APPLICATION NUMBER: 60/237,768
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/ PRIOR FILING DATE: 2000-10-03
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/ PRIOR APPLICATION NUMBER: 60/231,498
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/ PRIOR FILING DATE: 2000-09-08
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/ NUMBER OF SEQ ID NOS: 207012
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/ SOFTWARE: FastSeq for Windows Version 4.0
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/ SEQ ID NO 17145
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/ LENGTH: 30820
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/ TYPE: DNA
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/ ORGANISM: Human
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US-09-949-016-17145

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	Best Local Similarity	51.2%;	Pred. No. 0.00054;		
	Matches 129;	Conservative	0;	Mismatches 123;	Indels 0; Gaps 0;
Qy	403	AGTTCGCACTCAAATCTACTCGTATACATAAGAACAATGGCACAAATAAAGAAC	462		
Db	6548	AGATATATATATATATATGTATATAGATATATATATATGTATATAGATATAAT	6607		
Qy	463	AATACTCAAATTGAAGAAAGGTTCAANTGGTGCCCTAATATATGTAGACATTTTAGAAT	522		
Db	6508	ATATTATATATTGATATATAGATATATATATATATATATATATATATATATATATTT	6667		



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US-08-916-4218-1

Query Match 2.1%; Score 51.2; DB 4; Length 1664976;  
Best Local Similarity 44.9%; Pred. No. 0.076;  
Matches 240; Conservative 0; Mismatches 288; Indels 6; Gaps 1;

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Db TTTCTTCTATTTTAAATTTTCCAACTTTTATTAATTTCTATATAAACCTTTATCCATT 248094

Qy 2018 TAAATTTTATGTCAGCAATGCCAACTTTTATGCTGTCACCTTATAGCACAAAAC 2077  
Db AAATCACCAGTTGCCATATATAAATTTTAACTTTTAACTTTTATAGAAATAATTT 248034

Qy 2078 TATATCATTTTCTAATAGTCTTGAAATCCACATCTTATTTTAGCCTTTCTCAAAAT 2137  
Db TAAAGTATTTTATAGGTATCCATTTCAACTATATAAAATTTCTCTGTTTACAGGTAT 247974

Qy 2138 TGGCACAAAAC TAGGAAAATTTAATACATTTCTGCCATACACATATTTCTAGTGCNAATGTT 2197  
Db TGCTTAAATTTTAAATTTTATATAGTTTATATAAATAAATTTTGT-----ATAATTT 247920

Qy 2198 AACTAGATTTGCTCAATATTAGCAAACTTTTGTAGATTTCAATTAATTTGCTACATTTG 2257  
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Qy 2258 CATATCTTTTATAGAAATTTCAATATGCTTCAATAGCATCTTCAATTTTATGGAACCTTG 2317  
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Qy 2318 ATTAAACCCCTTAAATATAGCCAGTGCAGGATCCATTTAAAGGTGATTTCTTAATTT 2377  
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Qy 2438 TACACCACTACCCACACGTTGGACATATATATGAAAAATAGCTTCCACAGTCTA 2491  
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RESULT 5  
US-09-692-570-1/c  
Sequence 1, Application US/09692570  
Patent No. 6797466  
GENERAL INFORMATION:  
APPLICANT: Rult et al.  
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus  
FILE REFERENCE: PB275C1  
CURRENT APPLICATION NUMBER: US/09/692,570  
CURRENT FILING DATE: 2003-01-14  
PRIOR APPLICATION NUMBER: US 60/024,428  
PRIOR FILING DATE: 1996-08-22  
PRIOR APPLICATION NUMBER: US 08/916,421  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 1  
LENGTH: 1664976  
TYPE: DNA  
ORGANISM: Methanococcus jannaschii  
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; OTHER INFORMATION: n equals a, t, c, or g

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Query Match 2.11; Score 51.2; DB 4; Length 1664976;  
Best Local Similarity 44.91; Pred. No. 0.076;

Matches	240;	Conservative	0;	Mismatches	288;	Indels	6;	Gaps	1;
Qy	1958	TTTGTTAGTATGTTGTATATAAAAAATAATTTCTCTCTCTTTTGTGCACATCCAAATATTGACT	2017						
Db	248153	TTTTCTCAATTTTAAATTTTCAACCTTTTTTATTAATTTCTATAAAACCTCTTATCCAAAT	248094						
Qy	2018	TAAATTTTTATGTAGCAATGCCAACTTTTTTATGTAGTGTGCCACTTTATAGCACAAAAAC	2077						
Db	248093	AAATCACCAATGCCAATATAAATTTTTTAATCTTTTAACTATTTATAGAAATATTT	248034						
Qy	2078	TATATCCATTTTCTAATPAGTCTTGAATCCAATCTTAATTTTTTAGCCATTTCTCAAAAT	2137						
Db	248033	TAAAGTATTTATTAGTATGCCAATCAACTATATAAAAAATTTCTACTGATTCAGGTATAT	247974						
Qy	2138	TGCGACAAATCTAGGAAATTTAATACATTTCTTGCCATAACATATTTCTAGTGCAAATGTT	2197						
Db	247973	TGCTTAAAAATTTTAAATTTTTTATATAGTTTAAATATAAAATTTGT-----ATAATTT	247920						
Qy	2198	AAC TAGATGCTCAATATAGCAAACTTCTTTGTGAAGATTCATTAATATGCTACATGTG	2257						
Db	247919	AAATATATAGTGAATAATGAATTTAATATTAACCTACTACTCAATATTTTGCCATAAT	247860						
Qy	2258	CATACATTTTTTAGAAGTTTCATCAATATGCTCATTAGCATACTTCATTTTAGGAACTTG	2317						
Db	247859	GGCTTTTAAATTTTAAATTTTTTGTGGAATTTGGCTGATAAAAAACCTCTTATTTCCAAAAAG	247800						
Qy	2318	ATTAAACCGCTTTAAATATAGACGCAAGTCACGGATCCAATTTAAAGGTGAATTTCTTAATTT	2377						
Db	247799	AGCCAAAACCATATCAAGTTAGACATGGAAGCTCATCAAGTAAAGAGGTTATGGAAGT	247740						
Qy	2378	CTTACTTCCTATCTTTGGTGGCTTANGTTTTATATANGTGTGGGTGGTGAATGATGTCC	2437						
Db	247739	CATGATGTTTATCATCACCATATATGTAACATAAAGATGTCTANGTCCCAAGATATGCGGAT	247680						
Qy	2438	TACACCATCTACACCAACGTTGGACATATATATGGAATAATAGCTTCCACAGTCTA	2491						
Db	247679	GAGGACATTTATGATGAAGAGGAAAAAAGAGGGGTATAAAGATGATAGTTTAA	247626						

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RESULT 6
US-09-949-016-30530/c
; Sequence 30530, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30530
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-30530

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Query Match	1.98;	Score 48.2;	DB 4;	Length 601;
Best Local Similarity	51.17;	Pred. No. 0.0047;		
Matches 113;	Conservative	0;	Mismatches 108;	Indels 0; Gaps 0;
QY	429	ATACATPAAAGAAACATCGGACAAAAATTAAGAAACAATACTCAAAATATATGAAAAAGTTTCA	488	
Db	380	ATATATPAAAAATATATTTATATATATTTTAAATATATAATATATATATATATATATATATATAT	321	
QY	489	AATGGTGCTCTATAATTTATTTGTAGACATTTTGAAGATTTTATTTTAGACCAAAACACATTTAAAT	548	

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Db		
549	TTGGTTTAAAAACAGTTAGATATTAAATATTATTTCAGTTTATAGTTTATTTCGGACATTTTA	608
Qy		
260	ATATTATATATATTTTAAATATAAATATATAAATATATTTATATATATTTTAAATATA	201
Db		
609	TTTACTTAACTATACCTTCAGGCTTTTAAAGTAAATTTT	649
Qy		
200	AAATATATAAATATATATTTATATATATATTTTAAATATAAATAT	160
Db		

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RESULT 7
US-09-949-016-30531/c
/ Sequence 30531, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIORITY FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 30531
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-30531

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RESULT 8  
US-09-949-016-37149/c  
; Sequence 37149, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03

[illegible]





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Qy 609 TTACTTAATCTACTCTAGGGTTTAAAGTAAATTTT 649  
Db 200 AATATAAATAATATTTATATATATTTTAAATATAAATAT 160

## RESULT 15

US-09-949-016-146136/c  
; Sequence 146136, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCES: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: Pest-Seq for Windows Version 4.0  
; SEQ ID NO 146136  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-146136

Query Match 1.9%; Score 48.2; DB 4; Length 601;  
Best Local Similarity 51.1%; Pred. No. 0.0047;  
Matches 113; Conservative 0; Mismatches 108; Indels 0; Gaps 0;  
Qy 429 ATACATAAGAAACATGGGCACAAAATAAGAAACATCTCAAAATTTAGAAAAGTTCA 488  
Db 470 ATATATAAAATATATTTATATATATTTTAAATATAAATATAAATATAAATATA 411  
Qy 489 AATGGCTCTAATATTTAGACATTTTAGCAATTTTAAAGTAAATTTTAAAT 548  
Db 410 ATTTTAAATATAAATATAAATATAAATATAAATATAAATATAAATATAAAT 351  
Qy 549 TTGGTTTAAATAGTAGATATTAATATTTTTCAGTTTATAGTTATTTGGGACATTTA 608  
Db 350 ATATTTATATATTTTAAATATAAATATAAATAATATAAATATAAATATAAATATA 291  
Qy 609 TTACTTAATCTACTCTAGGGTTTAAAGTAAATTTT 649  
Db 290 AATATAAATAATATTTATATATATTTTAAATATAAATAT 250

Search completed: April 9, 2005, 07:59:45  
Job time : 438 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 20:49:49 / Search time 1154 Seconds  
(without alignments)  
12788.488 Million cell updates/sec

Title: US-10-089-612-2

Perfect score: 2493

Sequence: 1 agctttccggtgatgaag.....aaatgcttcacagctctaga 2493

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: N\_Geneseq\_16Dec04.\*
- 2: Geneseqn1980s.\*
- 3: Geneseqn1990s.\*
- 4: Geneseqn2000s.\*
- 5: Geneseqn2001as.\*
- 6: Geneseqn2001bs.\*
- 7: Geneseqn2002as.\*
- 8: Geneseqn2002bs.\*
- 9: Geneseqn2003as.\*
- 10: Geneseqn2003bs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2493	100.0	2493	4 AAF80481	AAF80481 Nucleotid
2	499	20.0	499	4 AAF80484	AAF80484 Nucleotid
3	341	13.7	1708	4 AAF80482	AAF80482 Nucleotid
4	339	13.6	507	4 AAF80485	AAF80485 Nucleotid
5	236.8	9.5	1232	4 AAF80483	AAF80483 Nucleotid
6	216.2	8.7	265	4 AAF80486	AAF80486 Consensus
7	163.6	6.6	531	4 AAF80480	AAF80480 Nucleotid
8	62	2.5	8056	8 ABZ10246	ABZ10246 Haematopo
9	60.4	2.4	10439	6 AAD47817	AAD47817 Alternati
10	60.4	2.4	11779	6 AAD42891	AAD42891 Maize sug
11	58.8	2.4	8056	8 ABZ10100	ABZ10100 Haematopo
12	55.6	2.2	2000	8 ADA71938	ADA71938 Rice gene
13	53.2	2.1	6863	4 AAS46617	AAS46617 Tumour su
14	52	2.1	12669	6 ABK31523	ABK31523 Signal tr
15	52	2.1	12669	6 ABL70450	ABL70450 Chemical
16	52	2.1	12669	6 AAS61449	AAS61449 Human gen
17	51.8	2.1	5252	6 ABL33135	ABL33135 Human inm
18	51.8	2.1	9810	6 ABL32426	ABL32426 Human inm
19	51.4	2.1	12142	6 ABL33673	ABL33673 Human inm
20	51.2	2.1	347	4 AAI87539	AAI87539 Human pol

c 21	51.2	2.1	110000	2 AAV21209-02	Continuation (3 of
c 22	51	2.0	15548	6 ABL34155	ABL34155 Human inm
c 23	50.6	2.0	7924	6 ABK40070	ABK40070 Human che
c 24	50.6	2.0	7924	6 ABL34139	ABL34139 Human inm
c 25	50.4	2.0	13377	4 AAS46476	AAS46476 Tumour su
c 26	50.4	2.0	13377	6 ABL33463	ABL33463 Human inm
c 27	50.2	2.0	5488	6 ABL33456	ABL33456 Human inm
c 28	50.2	2.0	33734	13 ABD12715	ABD12715 Human can
c 29	50	2.0	4001	13 ADS89759	ADS89759 Oligonuc1
c 30	50	2.0	8900	13 ADS89686	ADS89686 Oligonuc1
c 31	50	2.0	34688	6 ABQ67060	ABQ67060 Human ang
c 32	49.8	2.0	7442	4 AAS46686	AAS46686 Tumour su
c 33	49.6	2.0	113515	6 ABL34175	ABL34175 Human inm
c 34	48.8	2.0	2000	6 ABZ17152	ABZ17152 Arabidops
c 35	48.8	2.0	4045	4 AAS46740	AAS46740 Tumour su
c 36	48.8	2.0	5238	6 ABL32758	ABL32758 Human inm
c 37	48.8	2.0	110000	8 AAS53224-2	Continuation (3 of
c 38	48.6	1.9	5666	6 AAS61186	AAS61186 Human gen
c 39	48.6	1.9	5666	6 ABL49329	ABL49329 Human pol
c 40	48.4	1.9	4001	13 ADS89485	ADS89485 Oligonuc1
c 41	48.4	1.9	6167	6 ABK28370	ABK28370 DNA trans
c 42	48.4	1.9	6534	6 ABL32470	ABL32470 Human inm
c 43	48.4	1.9	8900	13 ADS89412	ADS89412 Oligonuc1
c 44	48.4	1.9	83391	6 ABQ67093	ABQ67093 Human ang
c 45	48.2	1.9	50000	6 ABL55643	ABL55643 AmSPV gen

## ALIGNMENTS

RESULT 1  
AAF80481  
ID AAF80481 standard; DNA; 2493 BP.  
XX  
AC AAF80481;

29-JUN-2001 (first entry)

Nucleotide sequence of the promoter of the Ear2 gene of maize.

Promoter; Ear2 gene; albumen; Angiosperm seed; embryo development;  
transgenic plant; seed starch; seed oil; food; ss.

Zea mays.

FR2799203-AL.

06-APR-2001.

01-OCT-1999; 99FR-00012305.

01-OCT-1999; 99FR-00012305.

(BIOG-) BIOGEMMA GAS.

Bonello JF, Rogowsky P, Perez P;

WPI; 2001-275283/29.

New plant promoters providing albumen-specific expression, useful for  
preparing transgenic plants with altered starch and oil contents.

Claim 3; Page 41-42; 47pp; French.

The present sequence represents a promoter of the Ear2 gene of maize. The  
promoter provides expression of attached sequences that is specific to  
the region of albumen surrounding the embryo in angiosperm seeds and  
active in the early stages of albumen development. The promoter provides  
specific expression of genes at an early stage of embryo development,  
resulting in seeds of increased size, enriched in starch and/or oil, or  
embryo-free seeds. The promoter is used to prepare expression cassettes  
for preparation of transgenic Angiosperm plants with improved agronomic  
or nutritional properties. Especially, these plants produce seeds with

CC	altered starch and oil contents and are useful as sources of human and
CC	animal foods
XX	
SQ	Sequence 2493 BP; 738 A; 430 C; 597 G; 728 T; 0 U; 0 Other:
	Query Match 100.0%; Score 2493; DB 4; Length 2493;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AAGCTTTTCGGGTGATGAAGCACCTGTAATACAGCATGCTCAAAACAATAGTTA 60
DB	1 AAGCTTTTCGGGTGATGAAGCACCTGTAATACAGCATGCTCAAAACAATAGTTA 60
QY	61 GCTGTGTTTTGAGGACCTTGGGAAGATGAAGGCCCCCAACACATCCCATGATCAAGTC 120
DB	61 GCTGTGTTTTGAGGACCTTGGGAAGATGAAGGCCCCCAACACATCCCATGATCAAGTC 120
QY	121 CCCATGACTTGCAAAAGCAAAATTTTATCAAAATTTCTCATAAACACTTCAAAACATT 180
DB	121 CCCATGACTTGCAAAAGCAAAATTTTATCAAAATTTCTCATAAACACTTCAAAACATT 180
QY	181 TCTCTTTTGAAGGTGTAGAGCACTAGCAACTGCTCTAATAAAGGTTCCCAAAATTTCT 240
DB	181 TCTCTTTTGAAGGTGTAGAGCACTAGCAACTGCTCTAATAAAGGTTCCCAAAATTTCT 240
QY	241 GGGTATAACAATCGCATGCTTAATAACAAGGAAATCTTACTAGAGCAGTAATTTGG 300
DB	241 GGGTATAACAATCGCATGCTTAATAACAAGGAAATCTTACTAGAGCAGTAATTTGG 300
QY	301 CTAAACAAATAGTGCATTTTAAATAGGAAATAGGAGCATGCAATCTGTGTTTC 360
DB	301 CTAAACAAATAGTGCATTTTAAATAGGAAATAGGAGCATGCAATCTGTGTTTC 360
QY	361 TTTTCAGGGTTTGTATGTCCTCAAAAGTGTGCCCTCGGGCAGTGTGCAACACTCAAAAT 420
DB	361 TTTTCAGGGTTTGTATGTCCTCAAAAGTGTGCCCTCGGGCAGTGTGCAACACTCAAAAT 420
QY	421 CTACTGTTATCATATAAGCAATAGGCAAAATTAAGAAACAATATCTCAAAATTAAGAA 480
DB	421 CTACTGTTATCATATAAGCAATAGGCAAAATTAAGAAACAATATCTCAAAATTAAGAA 480
QY	481 AAGGTTCAAAATGGTCTATATAATTTATGTAGACATTTTAAAGATTTATTTAGACCAAAACC 540
DB	481 AAGGTTCAAAATGGTCTATATAATTTATGTAGACATTTTAAAGATTTATTTAGACCAAAACC 540
QY	541 ATTAAATTTGGTTTAAATAGATTTAGATATAATTTATTTCAATTTATAGTTAATTTGG 600
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DB	601 GACATTTATTTACTTAATATACTTCTAGGGTTTAAAGTAAATTTTGGGTCCTTAGT 660
QY	661 TGGACTAGCTCAGATTTGCTGTTGATTTTCCATAAAGTCCAGGTTCTTTTAGCAAAAT 720
DB	661 TGGACTAGCTCAGATTTGCTGTTGATTTTCCATAAAGTCCAGGTTCTTTTAGCAAAAT 720
QY	721 CCAAGGTGAACAAAGGGGAGATAGGTGTTGACCGATATCTCTAAATTTGATCGTTGAC 780
DB	721 CCAAGGTGAACAAAGGGGAGATAGGTGTTGACCGATATCTCTAAATTTGATCGTTGAC 780
QY	781 GGCACATGATGCTCTCAGATTTAAATGGTGGATGTGCAAGCGACGCGACACGATGAGGA 840
DB	781 GGCACATGATGCTCTCAGATTTAAATGGTGGATGTGCAAGCGACGCGACACGATGAGGA 840
QY	841 ATGGCTCTACGACGGTGGCTACTAGAGCTGGCTAGCTCAACCAATGGGGCTCGGTCA 900
DB	841 ATGGCTCTACGACGGTGGCTACTAGAGCTGGCTAGCTCAACCAATGGGGCTCGGTCA 900
QY	901 AGGTCAAAATTTGTTGCCAAGCCAATGTTGGCTCAGATGAGTCCGATTTAGGACATATCAA 960
DB	901 AGGTCAAAATTTGTTGCCAAGCCAATGTTGGCTCAGATGAGTCCGATTTAGGACATATCAA 960

QY	961 GGTGAGGGTCAACAGAGGGGCAAGATCGATGGTGCAATGGTGTCTCGATGAAGGGG 1020
DB	961 GGTGAGGGTCAACAGAGGGGCAAGATCGATGGTGCAATGGTGTCTCGATGAAGGGG 1020
QY	1021 AAGCTTCGGGTGAGCAATTCAGATTTTCTATCATGTGCAACGGGTCAAGGAAATGGGCCAT 1080
DB	1021 AAGCTTCGGGTGAGCAATTCAGATTTTCTATCATGTGCAACGGGTCAAGGAAATGGGCCAT 1080
QY	1081 GGGGTTTGTGATGCTTCTGTCACATCATGTTGCTGTATCGATGTCAGGGAGCATTAGG 1140
DB	1081 GGGGTTTGTGATGCTTCTGTCACATCATGTTGCTGTATCGATGTCAGGGAGCATTAGG 1140
QY	1141 GTTCCACAGTCAGCGATGCAACGGCATGTGTGGCATTTGTGTCACTGTTGATCAACTA 1200
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QY	1201 GGGAGCATAGAGCTCTATGAAATTTTCACTTCTTCACTCTAGGATCATGTGACCA 1260
DB	1201 GGGAGCATAGAGCTCTATGAAATTTTCACTTCTTCACTCTAGGATCATGTGACCA 1260
QY	1261 AAGGTGGGAGGAGCGGGGCTCTCTAGTGAGGGTGGAAATGCACTGTCAGTGGGAAT 1320
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QY	1321 AGTGGCGCATCGCTTGTGTAATGAAATAGGTTGCTTGGGTGGCTGGGAGTGCATATGA 1380
DB	1321 AGTGGCGCATCGCTTGTGTAATGAAATAGGTTGCTTGGGTGGCTGGGAGTGCATATGA 1380
QY	1381 GGGAAATAGTTGGTGGCGGATGTTTCTTTTAAAGGAGCACATTTGATTAATGGAAGA 1440
DB	1381 GGGAAATAGTTGGTGGCGGATGTTTCTTTTAAAGGAGCACATTTGATTAATGGAAGA 1440
QY	1441 CAATGACACAAAGGGTGGGACAGTTTAAAGCTCGAATGCTGTAGGGGTGCTCAAGG 1500
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QY	1561 GGTGATGGGACAAAGGTAGTGTCTCAAGCAAGGAGGGGCGAGTTACAGCGCAGAGATGCT 1620
DB	1561 GGTGATGGGACAAAGGTAGTGTCTCAAGCAAGGAGGGGCGAGTTACAGCGCAGAGATGCT 1620
QY	1621 GTTGTGACACATGGGGGGGGGGAATTTGAGAGTTGGGGTTGACCAAGTGAATTTATGGG 1680
DB	1621 GTTGTGACACATGGGGGGGGGGAATTTGAGAGTTGGGGTTGACCAAGTGAATTTATGGG 1680
QY	1681 TGACCCAGAGAGAGAGACCCCACTGATGGGGGAAAGAGGTGCCAACAGGTGGGGACCAAGGT 1740
DB	1681 TGACCCAGAGAGAGAGACCCCACTGATGGGGGAAAGAGGTGCCAACAGGTGGGGACCAAGGT 1740
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DB	1741 GTCAGTGAATCAGCGTGACATGTTATTTGGAAGTTACGTCGGGAATGGTTGGGCTCGAG 1800
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FT		4481. .4588		XX		
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FT	intron	/number= 7		XX		
FT		4589. .4706		PR	24-MAR-1995; 95US-00410784.	
FT		/tag= q		XX		
FT	exon	/number= 7		XX	(IOHA ) UNIV IOWA STATE RES FOUND INC.	
FT		4707. .4792		XX		
FT		/tag= r		PI	Myers AM, James MG;	
FT	intron	/number= 8		XX	WPI; 2002-616514/66.	
FT		4793. .5062		DR		
FT		/tag= s		XX		
FT	exon	/number= 8		XX		
FT		5063. .5134		PT	Novel starch debranching enzyme protein sugary1 or its polypeptide	
FT		/tag= t		PT	fragment useful as replacement for bacterial and fungal enzymes currently	
FT	intron	/number= 9		XX	used in starch processing industry.	
FT		5135. .5206		PS	Claim 27; Col 41-52; 75pp; English.	
FT		/tag= u		XX		
FT	exon	/number= 9		CC	The invention relates to maize starch debranching enzyme, sugary1 (SUI)	
FT		5207. .5333		CC	and nucleic acid molecules encoding such proteins. SUI sequences are used	
FT		/tag= v		CC	as a replacement for the bacterial and fungal enzymes currently used in	
FT	intron	/number= 10		CC	the starch processing industry and as immunogens to raise antibodies for	
FT		5334. .7041		CC	against SUI. Polynucleotides of the invention are useful as markers for	
FT		/tag= w		CC	identification of specific corn varieties, for the development of corn	
FT	exon	/number= 10		CC	varieties with starch properties tailored for specific industrial	
FT		7042. .7128		CC	applications. The present sequence is maize SUI gene. Note: This sequence	
FT		/tag= x		CC	is stated to be the same as that shown as SEQ ID NO:3 (AAD47817) in	
FT	intron	/number= 11		CC	figure 2 of the specification. However the sequences differ	
FT		7129. .7902		XX		
FT		/tag= y		SQ	Sequence 11779 BP; 3264 A; 2538 C; 2418 G; 3559 T; 0 U; 0 Other;	
FT	exon	/number= 11				
FT		7903. .7995				
FT		/tag= z				
FT	intron	/number= 12				
FT		7996. .8429				
FT		/tag= aa				
FT	exon	/number= 12				
FT		8430. .8588				
FT		/tag= ab				
FT	intron	/number= 13				
FT		8589. .8811				
FT		/tag= ac				
FT	exon	/number= 13				
FT		8812. .8895				
FT		/tag= ad				

RESULT 11

AB210100/c  
ID AB210100 standard; DNA; 8056 BP.  
XX  
AC AB210100,  
XX  
DT 16-JAN-2003 (first entry)  
XX  
DB Haematopoietic cell proliferation disorder related DNA sequence #240.  
XX  
XX Human; haematopoietic cell proliferation disorder; cytostatic;  
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
KW cytosine methylation state; gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO20027272-A2.  
XX  
XX 03-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-EP003401.  
XX  
XX 26-MAR-2001; 2001US-0278333P.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Berlin K, Braun A, Dietler J, Gueig D, Howe A, Mueller J;  
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Liu E;  
PI Lewin A, Lipscher E, Maier S, Model P, Mueller V, Otto T, Pelet C;  
PI Schwoppe I, Ziebarth H;  
XX  
DR WPI; 2003-018942/01.  
XX  
XX Detecting and differentiating between hematopoietic cell proliferative  
PT disorders, comprises contacting a target nucleic acid with a reagent that  
PT distinguishes between methylated and non-methylated CpG dinucleotides.  
XX  
XX Claim 28; SEQ ID NO 240; 117pp; English.  
XX  
XX The present invention describes a method for detecting and  
CC differentiating between hematopoietic cell proliferative disorders  
CC associated with at least 1 gene and/or their regulatory regions in a  
CC subject. The method comprises contacting a target nucleic acid in a  
CC biological sample obtained from the subject with at least 1 reagent,  
CC which distinguishes between methylated and non-methylated CpG  
CC dinucleotides within the target nucleic acid. AS209661 to AS21118  
CC represent specifically claimed nucleotide sequences from the present  
CC invention. Oligonucleotides from the present invention can be used: for  
CC differentiating between healthy hematopoietic cells and proliferative  
CC disorder hematopoietic cells; for differentiating between acute  
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
CC determining the cytosine methylation state and/or single nucleotide  
CC polymorphisms (SNPs) of hematopoietic cell proliferation disorder  
CC related sequences and their complements; and as primers for the  
CC amplification of hematopoietic cell proliferation disorder related DNA  
CC sequences. The nucleotide sequences from the present invention can also  
CC be used for detecting a predisposition to, differentiation between  
CC subclases, diagnosis, prognosis, treatment and/or monitoring of  
CC haematopoietic cell proliferative disorders. The present method enables a  
CC highly specific classification of haematopoietic cell proliferative  
CC disorders allowing for improved and informed treatment of patients  
XX  
SQ Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;  
Query Match 2.4%; Score 58.8; DB 8; Length 8056;  
Best Local Similarity 45.1%; Pred. No. 0.0036;  
Matches 219; Conservative 0; Mismatches 267; Indels 0; Gaps 0;  
QY 1852 AATTGAAGTTGAATTTTAAATCAATCAATGATCTCCAAATCTCCAAATTTACCAA 1911  
DB 2361 AATTATATTTAAATTAATTAATTTTAAATGACGAAATTAATTAATTTAA 2302  
QY 1912 ATATGAATATTAGATGATATGTTGGTGAGTTTGGGCTCGCTTGTAGTAGTGT 1971

DB 2301 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2242  
QY 1972 TTGTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2031  
DB 2241 TTTTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2182  
QY 2032 GCATGCCCACTTTTGTAGTGTGACCTTATAGCACAATAAATAAATAAATAAATAA 2091  
DB 2181 ATAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2122  
QY 2092 AATAGTCTTGAATCCACATCTTATTTAGCCATCTTCAAAATTTGGCACAATAAATAA 2151  
DB 2121 AATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2062  
QY 2152 GAAATTTTAATACATTTCTGCCATAACATTTCTAGTGCAATATGTTAACTAGATTGCTCA 2211  
DB 2061 TTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2002  
QY 2212 ATATTAGCAAACTCTTTGTAGATTCATTAATATTGCTACATTTGCTACTTTTATGA 2271  
DB 2001 AAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1942  
QY 2272 AGTTCATCAATAATGCTCTCATTTAGCATACTTCTATTTAGCACTTGAATAAACCCTT 2331  
DB 1941 ATATTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1882  
QY 2332 AATAAATA 2337  
DB 1881 AATAAATA 1876  
RESULT 12  
ID ADAT1938 standard; DNA; 2000 BP.  
XX  
AC ADAT1938;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice gene, SEQ ID 5263.  
XX  
KW plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
XX  
OS Oryza sativa.  
XX  
FN WO2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PP 22-JUN-2001; 2001WO-IB001105.  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri P, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
XX WPI; 2003-175290/17.  
XX  
XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
XX Claim 27; SEQ ID NO 5263; 899pp; English.  
XX  
XX The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that





OS Unidentified.  
 PN WO200202807-A2.  
 XX 10-JAN-2002.  
 XX 29-JUN-2001; 2001WO-EP007471.  
 XX 30-JUN-2000; 2000DE-01032529.  
 PR 01-SEP-2000; 2000DE-01043826.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2002-154758/20.  
 XX Nucleic acid, useful for diagnosis and therapy of diseases associated  
 PT with cell signaling e.g. cancer, comprises chemically modified genomic  
 PT sequences of genes associated with cell signaling.  
 XX  
 PS Claim 1; SEQ ID NO 380; 24pp + Sequence Listing; English.  
 CC The invention relates to a nucleic acid comprising a sequence of at least  
 CC 18 bases of a segment of chemically pretreated DNA of genes associated  
 CC with cell signaling. The activity of the modified sequences of the  
 CC invention may be described as cytostatic. The object of the invention is  
 CC to provide the chemically modified DNA of genes associated with cell  
 CC signalling, as well as oligonucleotides and/or PNA-oligomers for  
 CC detecting cytosine methylations, as well as a method which is  
 CC particularly suitable for the diagnosis and/or therapy of genetic and  
 CC epigenetic parameters of genes associated with cell signaling. The  
 CC chemically modified DNA provided by the invention is useful for diagnosis  
 CC and therapy of diseases such as solid tumours and cancer. The sequences  
 CC given in records ABL70111-ABL70626 represent chemically pre-treated  
 CC genomic DNA's of genes associated with cell signalling. Note: The  
 CC sequence data for this patent is not represented in the printed  
 CC specification, but is based on sequence information supplied by the  
 CC European Patent Office  
 XX  
 SQ Sequence 12669 BP; 3610 A; 224 C; 2687 G; 6148 T; 0 U; 0 Other;  
 Query Match 2.1%; Score 52; DB 6; Length 12669;  
 Best Local Similarity 45.3%; Pred. NO. 0.17;  
 Matches 230; Conservative 0; Mismatches 275; Indels 3; Gaps 1;  
 QY 143 ATTTATCAAAATTTCTCATAAACACTTGAAACACTTTCTCTTTTGGAAAAGTGTAGAG 202  
 DB 3300 ATATCCCAACACTTTTAAABAACTAAABACTAAATCAATCACTAAATTTCAAAATTTABAAA 3241  
 QY 203 CACTAGCACTGTCTACTAAAGAGTTCCTCAATTTCTGGGTATACATCCGATGGTAA 262  
 DB 3240 CCAAGCTCAACCAACCCGAAACCTCAAAATACAAAATTAACCTAAACGGTAATATTA 3181  
 QY 263 ATAAACAAGAAATCTCTACTAAGCAGTAAATTTGGCTAAACAACTAGTACGATTTT 322  
 DB 3180 ACACCTATATCCCAATATCCCACTTTAAABAACTATACAAAATA---ATTACTTA 3124  
 QY 323 AATGTAATAGGAATAGGAGCATGCAATACCTGTGTTCTTTGAGGGTTTGTGATCTCA 382  
 DB 3123 AACCTAAACAAACAAATACATAATTAATCAATTAATTAATTAATTAATTAATTAATTA 3064  
 QY 383 AAGTGTGCCCCCTGGGGCAGTTCACACACTCAAAATCTACTCGTATACATAAAGAAAC 442  
 DB 3063 ACAAAATAAACCTTCTCTAAACCAACAAACAAACAAACAAACAAACAAACAAACAAAC 3004  
 QY 443 ATGGGCAACAATTAAGAAACAATCTCAATTAATGAAGGTTCAATGGTCTCTAAT 502  
 DB 3003 ATCAAAAAAACTTTCCAAAAAAATTAATAAATTTTACAAAATCTAATTTCTACCTTTATA 2944  
 QY 503 TATTGTAGACATTTTACAAATTTTATAGACCAAAACCAATTTAAATTTGGTTTAAATGA 562  
 DB 2943 AATTTACCGATTCTAAABATTTTATATAATTAATTAATTAATTAATTAATTAATTAATTA 2884

QY 563 GTTAGATATTAAATTTATTTCAGTTTATTAGTTTATTGGGACATTTATTACTTTAACTATA 622  
 DB 2883 TATCTAAATTTTTCATTTTACATATATTTTAAATTTTATCCATATTTTATTATTATA 2824  
 QY 623 ACTTCTAGGGTTTAAAGCTAAATTTTG 650  
 DB 2823 ATTATTTATTTTAAATTAATTAATCTTCG 2796

Search completed: April 9, 2005, 02:57:34  
 Job time : 1158 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:00:44 ; Search time 10359 Seconds  
(without alignments)  
11661.247 Million cell updates/sec

Title: US-10-089-612-2

Perfect score: 2493

Sequence: 1 agctttccggtgatgaag.....aaatagcttcacagtctaga 2493

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.cm.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.ste.\*  
12: gb.sv.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2493	100.0	2493	6	AX111989 Sequence
2	2493	100.0	3542	6	ZMA251320 Zea mays
3	499	20.0	499	6	AX111992 Sequence
4	341	13.7	1708	6	AX111990 Sequence
5	341	13.7	1708	8	ZMA251319
6	339	13.6	507	6	AX111993 Sequence
7	236.8	9.5	1232	6	AX111991 Sequence
8	216.2	8.7	265	6	AX111994 Sequence
9	163.6	6.6	531	6	AX111988 Sequence
10	163.6	6.6	531	8	ZMA251318
11	77.6	3.1	203163	8	AF546188 Contiguou
12	76.4	3.1	81372	2	AC139056 Mus muscu
13	76.4	3.1	105035	2	AC145452 Zea mays
14	74	3.0	7218	6	I66494 Sequence 14
15	72.6	2.9	192816	2	AC148162 Zea mays
16	70.4	2.8	178657	2	AC148234 Zea mays
17	70	2.8	211974	2	AC150184 Zea mays
18	67.2	2.7	149227	2	AC146976 Zea mays
19	67.2	2.7	288479	2	AC146814 Zea mays

C 20	65.8	2.7	129466	2	AC148099	Zea mays
C 21	63.8	2.6	181249	2	AC148479	Zea mays
C 22	63.6	2.6	10856	8	AY146813	Zea mays
C 23	62.4	2.5	186998	2	CR388057	Danio rer
C 24	62.4	2.5	993	8	AY232485	Zea mays
C 25	62	2.5	8056	6	AX599046	Sequence
C 26	62	2.5	10839	8	AY146796	Zea mays
C 27	62	2.5	10853	8	AY146816	Zea mays
C 28	62	2.5	10854	8	AY146798	Zea mays
C 29	62	2.5	10854	8	AY146814	Zea mays
C 30	62	2.5	10854	8	AY146814	Zea mays
C 31	62	2.5	10854	8	AY146815	Zea mays
C 32	62	2.5	10855	8	AY146800	Zea mays
C 33	62	2.5	10856	8	AY146791	Zea mays
C 34	62	2.5	10856	8	AY146797	Zea mays
C 35	62	2.5	10856	8	AY146806	Zea mays
C 36	62	2.5	10858	8	AY146786	Zea mays
C 37	62	2.5	10858	8	AY146788	Zea mays
C 38	62	2.5	10858	8	AY146789	Zea mays
C 39	62	2.5	10858	8	AY146790	Zea mays
C 40	62	2.5	10858	8	AY146792	Zea mays
C 41	62	2.5	10858	8	AY146793	Zea mays
C 42	62	2.5	10858	8	AY146794	Zea mays
C 43	62	2.5	10858	8	AY146795	Zea mays
C 44	62	2.5	10858	8	AY146799	Zea mays
C 45	62	2.5	10858	8	AY146801	Zea mays

#### ALIGNMENTS

RESULT 1  
AX111989  
LOCUS AX111989 2493 bp DNA linear PAT 01-MAY-2001  
DEFINITION Sequence 2 from Patent WO0125439.  
ACCESSION AX111989  
VERSION AX111989.1 GI:13938897  
KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE 1  
AUTHORS Bonello, J.P., Rogowsky, P. and Perez, P.  
TITLE Plant seed endosperm-specific promoter  
JOURNAL Patent: WO 0125439-A 2 12-APR-2001;  
Biogemma (FR)  
FEATURES  
Location/Qualifiers  
1..2493  
/organism="Zea mays"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4577"

Query Match	100.0%	Score 2493;	DB 6;	Length 2493;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2493;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AAGCTTTTCGGTGATGAAGCACCCTGTAAATACCTTAACGAGCATGCTGAAAACAATAGTTA	60	
Db	1	AAGCTTTTCGGTGATGAAGCACCCTGTAAATACCTTAACGAGCATGCTGAAAACAATAGTTA	60	
Qy	61	GCTGTGTTTTTGAGGACCTTCGGAAGATGAAGCCCCCAACACATCCCATGATCATAGTC	120	
Db	61	GCTGTGTTTTTGAGGACCTTCGGAAGATGAAGCCCCCAACACATCCCATGATCATAGTC	120	
Qy	121	CCCATGATCTGCAAAAAGCAAAATTTTATCAAAATTTTCTATATAAATCCTTGAAAAACATTT	180	
Db	121	CCCATGATCTGCAAAAAGCAAAATTTTATCAAAATTTTCTATATAAATCCTTGAAAAACATTT	180	
Qy	181	TCTCTCTTTTCAAAAGTGTAGACCACTGTCTACTAAAAAGSTTCCCAAAATTTCT	240	

Db 181 TCTCTTTTGAAGGTGTAGAGCACTAGCAACTGTCTACTTAAAGAGGTTCCCAAAATTTCT 240  
Qy 241 GGGTATAACAATTCGATGTAATTAACAACAAGGAAATCCTACTAAGAGCAGTAATTTGG 300  
Db 241 GGGTATAACAATTCGATGTAATTAACAACAAGGAAATCCTACTAAGAGCAGTAATTTGG 300  
Qy 301 CTAACAATAGTAGCAATTTTAATTAATAGGGAATAGAGCAGTGCATCTCTGTGTTTC 360  
Db 301 CTAACAATAGTAGCAATTTTAATTAATAGGGAATAGAGCAGTGCATCTCTGTGTTTC 360  
Qy 361 TTTTCAGGGTTTGATGTCCTCAAAAAGTGTGCCCTCGGGCAGTTCGAACTCAAAAT 420  
Db 361 TTTTCAGGGTTTGATGTCCTCAAAAAGTGTGCCCTCGGGCAGTTCGAACTCAAAAT 420  
Qy 421 CTACTCGTATACATAAAGAAACATCGGCACAAAATAGAAACAACTACTCAAAATATGAAA 480  
Db 421 CTACTCGTATACATAAAGAAACATCGGCACAAAATAGAAACAACTACTCAAAATATGAAA 480  
Qy 481 AAGGTTCAAAATGCTCTATAATTAATTTAGACAAATTTTAAAGTAAATTTGGTCCCTAGT 660  
Db 481 AAGGTTCAAAATGCTCTATAATTAATTTAGACAAATTTTAAAGTAAATTTGGTCCCTAGT 660  
Qy 541 ATTAAATTTGGTTTAAATGAGTTAGATATTAATTTTATTCAGTTTATAGTTATTTGG 600  
Db 541 ATTAAATTTGGTTTAAATGAGTTAGATATTAATTTTATTCAGTTTATAGTTATTTGG 600  
Qy 601 GACATTTATTTACTTAATTAATTTCTAGGTTTAAAGTAAATTTGGTCCCTAGT 660  
Db 601 GACATTTATTTACTTAATTAATTTCTAGGTTTAAAGTAAATTTGGTCCCTAGT 660  
Qy 661 TGGAACTAGCTCAGATTTGCTGATTTCCATAAAGTCCGAGGTTCTTTAGCAAAAAT 720  
Db 661 TGGAACTAGCTCAGATTTGCTGATTTCCATAAAGTCCGAGGTTCTTTAGCAAAAAT 720  
Qy 721 CCAGGTGAACAGGGGGAGATAGGTGTGACCGATATCTCTAAATTTGATGCTGGAC 780  
Db 721 CCAGGTGAACAGGGGGAGATAGGTGTGACCGATATCTCTAAATTTGATGCTGGAC 780  
Qy 781 GGCACTAGGATGCTCAGATTTAAATGGTGAATGTGCAAGCAGCGCACACAGATGGAGA 840  
Db 781 GGCACTAGGATGCTCAGATTTAAATGGTGAATGTGCAAGCAGCGCACACAGATGGAGA 840  
Qy 841 ATGGCTTACGACGGGTGCTAGAGCTGGCTAGCTGACCAATGGAGGCTCGGTCA 900  
Db 841 ATGGCTTACGACGGGTGCTAGAGCTGGCTAGCTGACCAATGGAGGCTCGGTCA 900  
Qy 901 AGGTCAAAAATTTGTTGCCAAGCCTGTGGCTCACTGATGAGTCGATTTGAGCACATATCAA 960  
Db 901 AGGTCAAAAATTTGTTGCCAAGCCTGTGGCTCACTGATGAGTCGATTTGAGCACATATCAA 960  
Qy 961 GGTGAGGCTCAACAGAGGGGCAAGATCGATGGTGGCTGCTCGATGGAGGGG 1020  
Db 961 GGTGAGGCTCAACAGAGGGGCAAGATCGATGGTGGCTGCTCGATGGAGGGG 1020  
Qy 1021 AAATCTCGGTGAGCAATTCAGAAATTTCTATCATGTGACCGGGTCAGGGAATGGGCGAT 1080  
Db 1021 AAATCTCGGTGAGCAATTCAGAAATTTCTATCATGTGACCGGGTCAGGGAATGGGCGAT 1080  
Qy 1081 GGGGTTTGTGTACTTCTGTGTCACATCATGTGCTGTATCGATGTCAAGGAGCAATHAG 1140  
Db 1081 GGGGTTTGTGTACTTCTGTGTCACATCATGTGCTGTATCGATGTCAAGGAGCAATHAG 1140  
Qy 1141 GTTCACGATCAGCGGATGACGGGCTGTGTGTCACCAATGGTTCGATCAACTA 1200  
Db 1141 GTTCACGATCAGCGGATGACGGGCTGTGTGTCACCAATGGTTCGATCAACTA 1200  
Qy 1201 GGGAGATAGATCTATAGAGTTTCAAACTTCTCACACTCTAGGGATCATGTGACA 1260  
Db 1201 GGGAGATAGAGCTATAGAGTTTCAAACTTCTCACACTCTAGGGATCATGTGACA 1260  
Qy 1261 AAGGTGGGGAGGACGGGGCTCTCTAGTGAAGGGTGAATGCAAGTTCTGTCAAGTGGGAAT 1320  
Db 1261 AAGGTGGGGAGGACGGGGCTCTCTAGTGAAGGGTGAATGCAAGTTCTGTCAAGTGGGAAT 1320

Qy 1321 AGTGGCGGCATCGCTGTGTAAATGAATAAAGGTCTTTGGGTGGCTGGGAAGTGCATATGA 1380  
Db 1321 AGTGGCGGCATCGCTGTGTAAATGAATAAAGGTCTTTGGGTGGCTGGGAAGTGCATATGA 1380  
Qy 1381 GGGAGTGTGTGGTGGGGGATGTTCTTTTATAAGGGAGACCAATTTGATTAATGGAGA 1440  
Db 1381 GGGAGTGTGTGGTGGGGGATGTTCTTTTATAAGGGAGACCAATTTGATTAATGGAGA 1440  
Qy 1441 CAATGACACAAGAGGTGGTGGGACAGTTTAAAGTCGAATGTGCTAGGGGTGCTCAAGG 1500  
Db 1441 CAATGACACAAGAGGTGGTGGGACAGTTTAAAGTCGAATGTGCTAGGGGTGCTCAAGG 1500  
Qy 1501 TTAAGAATCAGGCATCAGGGAGGAAGCGAGGATTAATAATTTCTTTACTCCAGTTGTGG 1560  
Db 1501 TTAAGAATCAGGCATCAGGGAGGAAGCGAGGATTAATAATTTCTTTACTCCAGTTGTGG 1560  
Qy 1561 GGTGATGGGGACAAGGGTGTGTCTCAAGCAAGGGAGGGCGAGTTTCAGCGCAGAGATGGCT 1620  
Db 1561 GGTGATGGGGACAAGGGTGTGTCTCAAGCAAGGGAGGGCGAGTTTCAGCGCAGAGATGGCT 1620  
Qy 1621 GTTGTGACACATCGGGGGGGGGAATTCGAGGTTTGGGTTGACCAAGTCAAGTTATGGCG 1680  
Db 1621 GTTGTGACACATCGGGGGGGGGAATTCGAGGTTTGGGTTGACCAAGTCAAGTTATGGCG 1680  
Qy 1681 TGACCCAGAGAGAGACCCACTGATGGGGAAAAAAGGTGCGCAACAGGTGGGGACCAAGGT 1740  
Db 1681 TGACCCAGAGAGAGACCCACTGATGGGGAAAAAAGGTGCGCAACAGGTGGGGACCAAGGT 1740  
Qy 1741 GTCAAGTCACTCACTGTGACATGTTAATTTGGAAGTTACGTCCGGAAATGGTTGGGCTCGAG 1800  
Db 1741 GTCAAGTCACTCACTGTGACATGTTAATTTGGAAGTTACGTCCGGAAATGGTTGGGCTCGAG 1800  
Qy 1801 TGAATCTAGGCTGGCTGGGCACTGTGCTGATCTTTAATTTCTCATTTCCCAATTTAAGT 1860  
Db 1801 TGAATCTAGGCTGGCTGGGCACTGTGCTGATCTTTAATTTCTCATTTCCCAATTTAAGT 1860  
Qy 1861 TGAATTTTAAATCAAAATCAAAATCTCTCCAAAATCTCTCCAAAATATATAGAAAT 1920  
Db 1861 TGAATTTTAAATCAAAATCAAAATCTCTCCAAAATCTCTCCAAAATATATAGAAAT 1920  
Qy 1921 ATTATAGTGAATATGTTGGTGGAGTTTGGGCTCGCTTTGGTTAGTATGTTGTTATAAA 1980  
Db 1921 ATTATAGTGAATATGTTGGTGGAGTTTGGGCTCGCTTTGGTTAGTATGTTGTTATAAA 1980  
Qy 1981 AATAATTTCT 2040  
Db 1981 AATAATTTCT 2040  
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QY 2461 ACATATATATGGAATAGCTTCACAGTCTAGA 2493  
Db 2461 ACATATATATGGAATAGCTTCACAGTCTAGA 2493

RESULT 2  
ZMA251320 3542 bp DNA linear PLN 26-APR-2000  
LOCUS Zea mays Ear2 gene, 5' flanking region.  
DEFINITION A251320  
ACCESSION A251320  
VERSION A251320.1 GI:7657939  
KEYWORDS 5' flanking region; Ear2 gene.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1  
AUTHORS Bonello.J.F., Opsahl-Perstad,H.G., Perez,P., Dumas,C. and Rogowsky,P.M.  
TITLE Ear genes show different levels of expression in the same region of maize endosperm  
JOURNAL Gene 246 (1-2), 219-227 (2000)  
MEDLINE 20231747  
PUBMED 10767543  
REFERENCE 2 (bases 1 to 3542)  
AUTHORS Rogowsky,P.M.  
TITLE Direct Submission  
JOURNAL Submitted (24-NOV-1999) Rogowsky P.M., Reproduction et Developpement des Plantes, ENS-Lyon, 46 allée d'Italie, P-69364 Lyon Cedex 07, FRANCE

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Db 1110 GCTGTGTTTGGAGGACCTTCGGAAGATGAAGGCCCCCAACACATCCCATGTCATCAAGTC 1169

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QY 301 CTAACAACAATAGTGAAGCAATTTAAATGTAATAGGGAATAGGAGCATGCAATCTTGTGTC 360  
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QY 361 TTTTCAGGGTTTTCATGCTCTCAAAAGTGTGCCCCCTGGGGCAGTTGCAACATCAAAAT 420  
Db 1410 TTTTCAGGGTTTTCATGCTCTCAAAAGTGTGCCCCCTGGGGCAGTTGCAACATCAAAAT 1469

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QY 841 ATGGCTTCAAGCGGTGGCTACTAGAGCTGGCTACGTCAACCAATGAGGGGCTCGGTCA 900  
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 Db 3510 ACATATATATGGAATAATAGCTTTCACAGTCTAGA 3542

RESULT 3  
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 LOCUS Sequence 5 from Patent WO0125439.  
 DEFINITION AX111992  
 ACCESSION AX111992  
 VERSION AX111992.1 GI:13938900  
 KEYWORDS  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Sukesyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1  
 AUTHORS Bonello, J.F., Rogovsky, P. and Perez, P.  
 TITLE Plant seed endosperm-specific promoter  
 JOURNAL Patent: WO 0125439-A 5 12-APR-2001;  
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 Db 421 TGTGGGTGGTGAATGATGTTCTTACACCACTACACCAAGTGGACATATATATGGAA 480  
 Qy 2475 AATAGCTTCACTAGTCTAGA 2493  
 Db 481 AATAGCTTCACTAGTCTAGA 499





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clade; Panicoidae; Andropogoneae; Zea.
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REFERENCE
AUTHORS Bonello,J.P., Rogowsky, P. and Perez, P.
TITLE Plant seed endosperm-specific promoter
JOURNAL Patent: WO 0125439-A 7 12-APR-2001;
Biogenma (FR)
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2 AAGATTCAATTAATATGCTACATTCATCAATATGCTC 61
Oy 2291 ATTAGCATCTTCATTTAGGAACCTTGATTAACCCGCTTAAATAGACCAAGTACG 2350
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122 RATTCATTTAAAGTGAATCTTAAATTCCTACTCTCTTCTTCTTCTTCTTCTTCT 181
Oy 2410 ATATGTGTGGTGGTGAATGATGTTCTTACACCACTACACCACTACACCACTACAC 2469
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Oy 2470 TGGAAATAGCTTCACAGTCTAGA 2493
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242 YRGAATAGCTTCACAGTCTAGA 265
ORIGIN
RESULT 9
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DEFINITION Sequence 1 from Patent WO0125439.
ACCESSION AX111988
VERSION AX111988.1 GI:13936896
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Bonello,J.P., Rogowsky, P. and Perez, P.
TITLE Plant seed endosperm-specific promoter
JOURNAL Patent: WO 0125439-A 1 12-APR-2001;
Biogenma (FR)
FEATURES
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Best Local Similarity 84.0%; Pred. No. 8e-24;
Matches 220; Conservative 0; Mismatches 39; Indels 3; Gaps 3;
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Oy 2472 GAAATAGCTTCACAGTCTAGA 2493
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RESULT 10
LOCUS ZMA251318 531 bp DNA linear PLN 26-APR-2000
DEFINITION Zea mays Ear1 gene, 5' flanking region.
ACCESSION AJ251318
VERSION AJ251318.1 GI:7657937
KEYWORDS 5' flanking region; Ear1 gene.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Bonello,J.P., Opahl-Perstad,H.G., Perez,P., Dunae,C. and Rogowsky,P.M.
TITLE Ear genes show different levels of expression in the same region of maize endosperm
JOURNAL Gene 246 (1-2), 219-227 (2000)
MEDLINE 20231747
PUBMED 10767543
REFERENCE
AUTHORS Rogowsky,P.M.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-1999) Rogowsky P.M., Reproduction et
Developpement des Plantes, ENS-Lyon, 46 allée d'Italie, F-69364
Lyon Cedex 07, FRANCE
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ORIGIN
Query Match 6.6%; Score 163.6; DB 8; Length 531;
Best Local Similarity 84.0%; Pred. No. 8e-24;
Matches 220; Conservative 0; Mismatches 39; Indels 3; Gaps 3;
Oy 2233 AAGATTCAATTAATATGCTACATTCGA-TACTTTTAAAGTTCATCAATATGCTC 2291
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272 ACGATTAACTAGTATGTCCTCAGTCATTTGTTTGGCAGCTTCATCAATATGCTC 331
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Oy 2352 ATCCATTAAAGGTGATCTTAAATTCCTACTCTTCTTCTTCTTCTTCTTCTTCT 2411
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QY 2472 GAAATAGCTTTCACAGTCTAGA 2493
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Db 510 GAAATAGCTTTCACATCTAGA 531
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RESULT 11
AP546188 203363 bp DNA linear PLN 20-DEC-2002
LOCUS Contiguous genomic DNA sequence comprising the 19-kDa zein gene
DEFINITION family from Zea mays, complete sequence.
ACCESSION AP546188
VERSION AP546188.1 GI:25992761
KEYWORDS HTG.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 203363)
Song,R. and Messing,J.
Zein
Contiguous genomic DNA Sequence Comprising the 19-kD Zein Gene
Family from Maize
Plant Physiol. 130 (4), 1626-1635 (2002)
12481046
2 (bases 1 to 203363)
Song,R. and Messing,J.
Direct Submission
Submitted (12-SEP-2002) The Plant Genome Initiative at Rutgers -
Wakman Institute, Rutgers University, 190 Frelinghuysen Road,
Piscataway, NJ 08854-8020, USA
Zea mays (B73) BAC clone Z492M16 containing 19 kDa zein z1b
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ORIGIN
Query Match 3.1%; Score 77.6; DB 8; Length 203363;
Best Local Similarity 76.6%; Pred. No. 7.7e-06;
Matches 95; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 AGCTTTTCCGGTGAAGCAGCTGTTAATCTTAACAGCATGCTGGAACAAATAGTTA 60
6526 AGCGTTTTCGTGACAAAGCTCTGTATATTATTTAGTAGTAGCTTAAGCTAAAGCAATAGTTA 6585
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 GCTGTGTTTTGAGACCTTCGGAGATGAAGGCCCCCAACATCCCATCAATCAATGC 120
6586 GCATATTTTGGAGACCTTCGGAGATGAAGGCCCCCAACATCAATCAATCAATCTTCTT 6645
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 CCCA 124
6646 ACTA 6649
|||||

RESULT 12
AC139056 81372 bp DNA linear HTG 02-MAY-2003
LOCUS Mus musculus chromosome 15 clone RP23-17A19 map 15, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
ACCESSION AC139056
VERSION AC139056.2 GI:30315764
KEYWORDS HTG; PHASE0.
SOURCE Mus musculus (house mouse)

```

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 81372)

## AUTHORS

Birren,B., Nusbaum,C. and Lander,E.

## TITLE

Mus musculus chromosome 15, clone RP23-17A19

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 81372)

## AUTHORS

Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hages,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Menus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

## TITLE

Direct Submission

## JOURNAL

Submitted (23-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

## REFERENCE

3 (bases 1 to 81372)

## AUTHORS

Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hages,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Menus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

## TITLE

Direct Submission

## JOURNAL

Submitted (02-MAY-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

## COMMENT

On May 2, 2003 this sequence version replaced gi:27877333. All repeats were identified using RepeatMasker: Smit, A.P.A. &amp; Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submission@genome.wi.mit.edu

Center project name: L29023

Center clone name: 17\_A\_19

\*\*\*\*\*

\* NOTE: This record contains 80 individual

\* sequencing reads that have not been assembled into

\* contigs. Runs of N are used to separate the reads

\* and the order in which they appear is completely

\* arbitrary. Low-pass sequence sampling is useful for

- \* identifying clones that may be gene-rich and allows
- \* overlap relationships among clones to be deduced.
- \* However, it should not be assumed that this clone
- \* will be sequenced to completion. In the event that
- \* the record is updated, the accession number will
- \* be preserved.

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908 1006: contig of 899 bp in length
909 2005: gap of 100 bp
910 2861: contig of 856 bp in length
911 2862 2861: gap of 100 bp
912 3888: contig of 927 bp in length
913 3889 3888: gap of 100 bp
914 3889 3888: gap of 100 bp
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916 5040: gap of 100 bp
917 5973: contig of 933 bp in length
918 6074 5973: gap of 100 bp
919 6998: contig of 925 bp in length
920 7098: gap of 100 bp
921 8014: contig of 916 bp in length
922 8114: gap of 100 bp
923 9047: contig of 933 bp in length
924 9147: gap of 100 bp
925 10062: contig of 915 bp in length
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927 11090: contig of 928 bp in length
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Query Match 3.14; Score 76.4; DB 2; Length 81372;  
Best Local Similarity 84.34; Pred. No. 1.4e-05;

Matches 86; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy 1 AAGCTTTTCGGTGTGATGAGCCTGTATATCTTAACAGCATCTCAAAACAAATAGTTA 60
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Qy 61 GCTGTGTTTTTGAGGACCTTCGGAAGATGAGGCCCAACA 102
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RESULT 13  
AC145452/c

LOCUS AC145452 105035 bp DNA linear HTG 16-JUN-2004  
DEFINITION Zea mays clone ZMMB0016A01, \*\*\* SEQUENCING IN PROGRESS \*\*\*

ACCESSION AC145452

VERSION AC145452.7 GI:48717633

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.

SOURCE Zea mays

ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.

Center clone name: 16\_A.1  
----- Consensus Information  
This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above 020 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.  
-----  
\* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 105035: contig of 105035 bp in length.  
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FEATURES  
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103873 AGCTTTTCCGTCGATGACGACCTCTGAGTACTTAAACAGCATCTGGAACAAATAGTTA 103814  
61 GCTGTGTTTTCGACGACCTCTGAGTACTTAAACAGCATCTGGAACAAATAGTTA 102  
103813 GCTGTGTTTTCGACGACCTCTGAGTACTTAAACAGCATCTGGAACAAATAGTTA 103772

RESULT 14  
166494/c  
LOCUS 166494  
DEFINITION Sequence 14 from patent US 5670367.  
ACCESSION 166494  
VERSION 166494.1 GI:2724471  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 7218)  
AUTHORS Dörner, F., Scheiflinger, F. and Falkner, F. Gunter.  
TITLE Recombinant fowlpox virus  
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;  
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Location/Qualifiers  
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Best Local Similarity 9.0%; Pred. No. 4.9e-05;  
Matches 41; Conservative 234; Mismatches 179; Indels 0; Gaps 0;  
1286 AGTGAGGGTGAATGTCAGTTCTGTCACGTCGGGAAATAGTGGCGCATCGCTGTGAATGAAT 1345





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/db\_xref="taxon:4577"  
/clone="ZMHB0375A01"  
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Query Match 2.9%; Score 72.6; DB 2; Length 192816;  
Best Local Similarity 67.5%; Pred. No. 8.7e-05;  
Matches 102; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
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Db 142127 AACCTTTGTTTATGACGAAGCTCCTGTAATATTGACATTATGCTAGAAATTAATGGTTA 142068  
QY 61 GCTGTGTTTTTGGAGGACCTTCGGAAGATGAAGGCCCAACACATCCCATGCAATCAAGTC 120  
Db 142067 GTCGTGTTTTTGGAGGACCTTCGGAAGATGAAGGCCCAACACATCCCATGCAATCAAGTC 142008  
QY 121 CCCATGACTTGCMAAAAGCAATTTTATCA 151  
Db 142007 ATTATCATTGAACATTGCAAGAACTTTATTA 141977

Search completed: April 9, 2005, 05:51:59  
Job time : 10363 secs